

Fig 1. Genes Regulated by Diet ^a

GenBank	Other ID	Gene_Name	Predicted_Gene_Function
1915779	gb:L40631	Ank3	Ankyrin 3, epithelial
1310123	tr Q99M14	Ctss	Cathepsin S
2248057	tr Q920G6	Cd59a	CD59A
1497811	sp Q9JIF7	Copb1	Coatmer beta subunit
1357027	RFUG16661	C77823	Drosophila Crooked Neck Protein
1487297	tr Q91YZ0	Gabpb1	GA-binding protein transcription factor, beta subunit 1
1355364	pimr NF00559002	Pygb	Glycogen phosphorylase (EC 2.4.1.1), brain
1428425	RHUM231179	Ids	Iduronate 2-sulfatase (EC 3.1.6.13)
1555484	PMID: 10225949	Kif21b	Kinesin family member b21
1861860	tr Q99PB1	Mage-G2	Melanoma associated Antigen-g2
1938196	tr Q9BRH3	Pcolce2	Procollagen C-endopeptidase enhancer 2
1681368	gi 4322304	Eif5	Protein Translation Initiation Factor 5B (IF-5B)
1436357	LL: 66562	Pegpep1	Pyroglutamate-carboxylate/pyroglutamate peptidase I
1436776	pimr NF00568902	Rps18	Ribosomal protein S18; ERGO: SSU ribosomal protein S13P
1677535	LL: 68188	Spk	Symplekin
1715326	pir B39798	D7Rp2e	Testosterone-regulated RP2 protein
1915216	pimr NF00382654	Kras2	Transforming protein c-Ki-ras-1, hepatic
2164720	sp Q9JIQ8	Trmprs2	Transmembrane protease, serine 2 (EC 3.4.21.-)
1699544	tr Q91WM3	U3-55K	U3 snoRNP-associated 55-kDa protein
2202207	tr Q9H3P2	Whsc2h	Wolf-Hirschhorn syndrome candidate 2 protein

^a These genes may be used to determine nutritional status in any genotype

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Fig 2. Genes Regulated by Diet Depending Upon Genotype ^a

GenBank	Other ID	Gene_Name	Predicted_Gene_Function
1506585	IMAGE:3487719	Agpat1	1-acylglycerol-3-phosphate O-acyltransferase 1
1519882	tr Q99JE6	Pbpd	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta (EC 3.1.4.11)
1326479	pirnr NF00561668	Decr1	2,4-dienoyl-CoA reductase (NADPH2) (EC 1.3.1.34)
1738613	sp Q13200	9430095H01Rik	26S proteasome non-ATPase regulatory subunit 2
1649287	RMU001878	Ephx2	2-hydroxymuconic semialdehyde hydrolase (EC 3.7.1.9) (EC 3.3.2.3)
2050049	sp P16118	Pfkfb1	6-phosphofructo-2-kinase(EC 2.7.1.105)/Fruct-2,6-bisphosphatase(EC 3.1.3.46)
1539949	IMAGE:404058	Acat1	Acetyl-Co A acetyltransferase 1, mitochondrial,
1650569	tr Q8R2M2	C1qbp	Acidic 82 kDa protein mRNA - complement cascade
2049046	TR:G1217996	Adk	Adenosine Kinase
2181006	IMAGE:864557	Adat1	Adenosine deaminase, tRNA-specific 1
1494546	RGG00608	Adsl	Adenylosuccinate lyase (EC 4.3.2.2)
1484064	tr Q9Y360	AdipoR1	Adiponectin receptor 1
1700965	tr Q9J16	Aldr3	Alcohol dehydrogenase [NADP+] (EC 1.1.1.2); Aldr5
1504171	RRC03925	Aldh3A2	Aldehyde dehydrogenase (EC 1.2.1.3)
2192713	tr Q9PUF6	Pdgfrl	Alpha platelet-derived growth factor receptor (EC 2.7.1.112)
2308600	IMAGE:947971	Als2	Alsln
1446558	tr Q9UJX6	Anapc2	Anaphase-promoting complex subunit 2
2158093	tr Q9BQD4	Anapc5	Anaphase-promoting complex subunit 5
1309130	tr Q96FD5	Agt	Angiotensinogen
1380860	RHUM171320	Camta2	Ankyrin repeat proteins
1501085	pirnr NF00970234	Bat8	Ankyrin repeat-containing protein isoform b; NG36 protein
1749050	tr Q9UQ33	Trim21	APC-binding protein EB1
1807018	tr Q13786	ApoB100	Apolipoprotein B100
1294347	IMAGE:337401	Afrp1	ARF-related protein 1
2049140	IMAGE:751716	Carm1	Arginine methyltransferase
1655040	sp P56480	Atp5b	ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)
1650960	RHUM070757	Psmc1	ATP-Dependent protease subunit
2041641	RHUM110702	Ddx10	ATP-Dependent RNA helicase DDX10
1556028	sp Q9WU60	Atrn	Attractin precursor
1379831	sp Q99J83	Apq5l	Autophagy protein 5-like
1863019	sp O15169	Axin	Axin 1
1426777	RHUM131083	Elf3	Bacterial Protein Translation Initiation Factor 3 (IF-3)
2158175	IMAGE:847916	Bzw1	basic leucine-zipper protein BZAP45
1909198	sp Q9IA79	Tegt	Bax inhibitor-1

2140072	IMAGE:803897	Bspry	B-box and SPRY domain; Ro-RET family
1284468	sp Q9WU82	Catnb	Beta-catenin
1796473	gb:L20276	Bgn	Biglycan (MOUSE);
1542473	gb:M63725	Tcra	Binding protein for T-cell receptor (MOUSE);
1769161	tr Q8R0T3	Bing4	BING4 protein
1464229	tr Q91XB9	Bpnt1	Bisphosphate 3'-nucleotidase 1
1530059	IMAGE:476099	Spnb1	β -Spectrin
2075615	tr Q967Y2	Gli	C2H2 zinc finger transcription factor JING
2164107	IMAGE:865140	CAbin1	Calcineurin inhibitor mRNA
1310456	tr Q91YS8	Camk1	Calcium/calmodulin-dependent protein kinase I
1888270	sp Q9UDP3	S100a14	Calgizzarin
1660476	pirnr NF00412795	Calm3	Calmodulin
1447096	pirnr NF00046752	Calm1	Calmodulin
1862567	RMU006402	Calmbp1	Calmodulin-binding protein SHA1
2187828	tr Q8VCC8	Cgef2-pending	cAMP-regulated guanine nucleotide exchange factor I
1555146	tr Q96MP0	Ppap2a	Cavia porcellus phosphatidic acid phosphatase 2a
1650686	IMAGE:557633	Centb1	Cell membrane protein, recycling membrane
1356924	pirnr NF00965742	Pde6d	cGMP 3',5'-cyclic phosphodiesterase delta-subunit (EC 3.1.4.17)
1853138	IMAGE:670788	Cctb	Chaperonin containing TCP-1 eta subunit, CCT7
1529944	tr Q8QZW9	Ccrl1	Chemokine receptor CCX CKR
1909356	IMAGE:737955	Cldn14	Claudin 14; deafness
1676738	tr Q9UBD8	Cln3	CLN3 protein
2284153	tr Q9Z197	Myc	C-myc protein
2187172	sp Q9JIF7	Copb2	Coatamer beta subunit
1882128	IMAGE:717783	Ckn1	Cockayne syndrome group A (CSA gene)
1904767	IMAGE:733800	Dpysl5	Collapsin response mediator protein 5 (Crmp5)
1806950	tr Q8R099	C1s	Complement C1s component precursor (EC 3.4.21.42)
1483940	tr Q9R1A8	Cop1-pending	COP1 protein; photomorphogenic protein 1 (Arabidopsis)
1727163	tr Q8VDN0	Cox15	COX15 homolog, cytochrome c oxidase assembly protein
1357649	tr Q8R331	Rfx3	Cyclin G1 interacting protein
2200731	sp O14976	Gak	Cyclin G-associated kinase (EC 2.7.1.-)
1905747	tn AAH30473	Cars	CysteinyI-tRNA synthetase
2187717	RHUM131757	Cars	CysteinyI-tRNA synthetase (EC 6.1.1.16)
1910397	tr Q9D881	Cox5b	Cytochrome c oxidase, subunit Vb
2042539	sp Q9QZ82	Cyp11a	Cytochrome P450 11A1, mitochondrial precursor (EC 1.14.15.6)
1907861	tr Q9JJ02	Cyp29b	Cytochrome P450 2B9 (EC 1.14.14.1)
1902148	tr Q8VCP4	Cyp2c40	Cytochrome P450 2c40
1555555	pir S47553	Cyp4a10	Cytochrome P450 Cyp4a
2235102	IMAGE:920143	Ak1	Cytosolic adenylate kinase.

1445948	tr Q9BVD8	Dctd	dCMP deaminase
1357656	gi 3023156	Kns2	Decahistidyl-kinesin light chain
2187287	RMU003917	Rbp1	Deleted in split hand/split foot protein 1
1562575	IMAGE:482376	Dld	Dihydrolipoamide dehydrogenase
1834201	gb:D16373	1600017E01Rik	Dihydrolipoamide succinyltransferase component.
1862437	IMAGE:692981	Dhodh	Dihydroorotate dehydrogenase
1554403	RHUM171401	Dpep1	Dipeptidase (EC 3.4.-.-)
1841125	pirn NF00087367	NP_659138.1	dJ545L17.3 (proteasome (prosome, macropain) inhibitor subunit 1 (Pi31)
1676114	pirn NF00082232	Dffa	DNA fragmentation factor, 45 kD, alpha polypeptide
2308561	tr Q9WTM5	Helb	DNA helicase
1542146	IMAGE:420631	Xrcc1	DNA repair protein
1684156	tr Q9Y3R6	Rpc62	DNA-directed RNA polymerase III, subunit 4 (EC 2.7.7.6)
1904320	tr Q96FI3	Dpm2	Dolichyl-phosphate-mannose--protein mannosyltransferase (EC 2.4.1.109)
1505147	tr Q8R5K1	Dntnp	Dosal neuron-tube nuclear protein
1902535	tr Q9QUI6	Dfy	Duffy antigen/receptor for chemokine glycoprotein
1282761	RHUM020633	Dnclc2	Dynein 2 light intermediate chain
1446049	IMAGE:436886	Atp1a4	E1-E2 ATPase cellular membrane
2283419	sp Q9HC35	Mta111	Echinoderm microtubule-associated protein-like 4
1702212	RHS25959	Lre1	Endonuclease/reverse transcriptase
1357618	RHS19436	Serpinf1	EPC-1 - serpin, = serine protease inhibitor; Pigment epithelium-derived factor
1446754	pirn NF00062467	Efnb1	Ephrin B1
1429076	tr Q9WV79	Sc4mol	ERG2 protein
1328562	tr Q99LD9	Elf2b	Eukaryotic translation initiation factor 2B, subunit 2
2049576	tn AAK52330	Mapk1	Extracellular signal-regulated kinase 1 (EC 2.7.1.-)
2042313	IMAGE:570496	Fbxo6b	F-box protein FBX6b
2292384	pirn NF00017797	Fdx1	Ferredoxin, 2Fe-2s
2256866	sp P11276	Fn1	Fibronectin precursor
1630486	tr Q91ZX9	SFRP4	Frizzled-related protein 4
1746733	sp P39949	Ccne1	G1/S-specific cyclin E1
1475428	sp P41002	Ccnf	G2/mitotic-specific cyclin F.
1882008	gb:M96265	Galt	Galactose-1-phosphate uridyl transferase
2102585	tr Q8R590	Gsn	Gelsolin
1861211	pir A40467	Ugt1a1	Glucuronosyltransferase (EC 2.4.1.17) precursor
1811443	pir A35444	Gls	Glutaminase (EC 3.5.1.2), hepatic
1807028	gb:M77003	Gpam	Glycerol-3-phosphate acyltransferase
1897200	tr Q96N34	Gosr1	Golgi SNAP receptor complex member 1
1373801	gb:M58288	Csf1r	Granulocyte colony-stimulating factor receptor
1488749	RFUG00327	Ghr	Growth hormone secretagogue receptor type 1
1853004	tr Q91VC9	Tegt	Growth hormone-inducible membrane protein

1913128	IMAGE:764677	Ghitm	Growth hormone-inducible membrane protein mRNA
1711797	IMAGE:582932	M-Ras	GTPas involved in actin cytoskeleton
2164939	tr Q91X95	Gna11	Guanine nucleotide binding protein, alpha 11
1317824	tr Q9CWL5	Gngt2	Guanine nucleotide binding protein, gamma transducing activity polypeptide 2
1474674	IMAGE:442301	Vav2	Guanyl exchange protein
1751874	gb:M81128	Gbp2	Guanylate binding protein.
1464733	RFUG11345	Ubr1	HECT-domain ubiquitin-protein liages E3 (EC 6.3.2.-)
1776367	tr Q9ERZ0	Hemgn	Hemogen
1446915	tr Q9ERZ0	Hemgn	Hemogen (transcription factor)
1514269	sp P01944	Hba	Hemoglobin alpha chain
1895338	pirnr NF00110540	Hal	Histidine ammonia-lyase (EC 4.3.1.3); histidase
1676239	tr O15787	Hdc	Histidine decarboxylase (EC 4.1.1.22)
2196139	tr Q9NPA7	Hnrph3	hnRNP 2H9A;
1531123	RHUM11049	Hipk2	Homeodomain-interacting protein kinase 2 (EC 2.7.1.-)
1699768	tr Q8WW71	Hgd	Homogentisate 1,2-dioxygenase (EC 1.13.11.5)
2305949	tr Q9BVV7	Flot1	HSPC154 protein = flotilin 1
1283303	tr Q9BYW2	Hip1	Huntingtin interacting protein 1
1497254	tr Q9DBK1	Hmgcs2	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5)
1915278	IMAGE:748015	Imap38	Immunity associated immune function
1841024	tr Q91WX1	Rgs2	Implantation-related RGS2-like protein
1487112	tr Q9H2U2	Pyp	Inorganic pyrophosphatase (EC 3.6.1.1)
2192375	IMAGE:5026869	Iptk1	Inositol 1,3,4-triphosphate 5/6 kinase
1297504	pirnr NF00107717	Ilgb1bp1	Integrin cytoplasmic domain-associated protein 1
1755563	tr Q91VV8	Iag203	Interferon activated gene 203
1889604	tr Q9CTR9	Il6ra	Interleukin 6 receptor, alpha
2283227	IMAGE:945014	Clic4	Intracellular chloride channel protein
1500921	gi 6180179	AA030924	JM11 protein
1795172	tr Q91VM3	DXImx38e	JM5 protein 125kd membrane protein
1317814	RHS00933	Prnpip1	KAPD - B. subtilis, kinase
2306066	IMAGE:3672708	Kpna4	Karyopherin (importin) alpha 4
1509303	tr Q8R0Y0	Lamb2	Laminin, beta 2
1644096	pir A34260	Cyp43	laurate omega-hydroxylase (EC 1.14.15.3) cytochrome P450 4A5
1658728	IMAGE:556878	Mrc2	Lectin lambda
1285968	tr Q9NSE1	Lars	Leucyl tRNA synthetase
1509296	IMAGE:4504055	LGN	LGN protein
1861663	sp Q64176	Es1	Liver carboxylesterase 22 precursor (EC 3.1.1.1)
1555767	IMAGE:482626	Ly6g6c	Lymphocyte antigen complex 6
2057364	gb:D45859	Ppm1b	Magnesium dependent protein phosphatase
1932173	pirnr NF00499338	Mup2	Major urinary protein 2 precursor

2187377	IMAGE:871705	PPP3CA	Map kinase phosphatase-M A1
1853320	trIQ91VR7	Map1lc3	MAP1 light chain 3-like protein 1
2041342	spIQ9TUL9	Timp3	Metalloproteinase inhibitor 3 precursor
1294487	trIQ8R032	Gst2	Microsomal glutathione S-transferase 2
1527865	RFUG03427	Mcrs1	Microspherule protein 1
1529619	trIP82677	Rps27	Mitochondrial 28S ribosomal protein S27
2288329	pinrINF00092994	Slc25a20	Mitochondrial carnitine/acylcarnitine carrier protein
2235265	trIQ9N285	Mtch2	Mitochondrial carrier homolog 2
1558135	trIQ96G65	5730405E07Rik	Mitochondrial intermediate peptidase (EC 3.4.24.59)
1875338	trIQ924T2	Mrps2	Mitochondrial ribosomal protein S2
1474933	tnIAAH29784	Mrps30	Mitochondrial ribosomal protein S30
1676097	trIQ9WU4	Map4k4	Mitogen activated protein kinase kinase kinase (MAP4K4)
1557815	gb:D63902	Trim25	Mouse mRNA for estrogen-responsive finger protein
1464182	gb:M28821	Tcte1	Mouse T-complex-associated-testes-expressed-1
1375545	IMAGE:388264	Myadm	myeloid associated differentiation protein
2040121	trIQ96M12	Myadm	Myeloid associated differentiation protein
1840637	pinrINF00568678	Myjpc	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform
1660028	RHUM150245	Myo5a	Myosin Va
1937664	gb:S68616	Slc9a1	NA(+)/H(+) Exchanger1.
1934380	RRN03883	Ndufs6	NADH-ubiquinone oxidoreductase 13 kDa B subunit (EC 1.6.5.3) / (EC 1.6.99.3)
1407501	RHUM120137	Ndufb6	NADH-ubiquinone oxidoreductase subunit B17.2 (EC 1.6.5.3) / NADH dehydrogenase (EC 1.6.99.3)
1555757	trIQ9ERK2	Mell1	Neprilysin-like peptidase gamma
2271912	trIQ9ERK2	Mme	Neprilysin-like peptidase gamma
1325306	IMAGE:350863	Ncald	Neurocalcin delta
1435837	giJ5650693	Nefl	Neurofilament, light polypeptide
1285745	RMU004040	Nab2	NGFI-A binding protein 2 (EGR1-binding protein 2)
2202141	spIQ96PB7	Noelin	Noelin 3
2250161	tnIAAH28797	Nscn1	Non-selective cation channel 1
2049524	trIQ9ER19	Nulp1	Nuclear localized binding protein
2292188	trIQ9BTE9	Numa	Nuclear mitotic apparatus protein 1
2288782	spIQ00567	Nol5a	Nucleolar protein Nop56
1355494	trIQ9LIH8	Ncl	Nucleolin
1474962	spIQ90380	Nme2	Nucleoside diphosphate kinase (EC 2.7.4.6)
1446725	trIQ9WVG7	Osr1	Odd-skipped related 1 protein
2199776	spIP54370	Oazi	Ornithine decarboxylase antizyme
2076093	trIQ8QHL	Oazi	Ornithine decarboxylase antizyme inhibitor
1474562	trIQ96S44	Osgp	O-sialoglycoprotein endopeptidase (EC 3.4.24.57)
2041096	trIQ96NH5	Osgp	O-sialoglycoprotein endopeptidase (EC 3.4.24.57)

2041160	tr Q96SC6	Ott-Mal	OTT-MAL: RNA binding RRM domain
1371927	tr O44231	Dncl1	Outer arm dynein light chain 1
1659893	tr Q8WWA9	Cyp2d10	P450, progesterone 6 beta- and 16 alpha- hydroxylation activities plus others
1447198	IMAGE:437336	Pard6A	Partitioning defective protein
1427567	pirnr NF00030441	Tpo	Peroxidase: Thyroid peroxidase precursor (EC 1.11.1.8)
1463760	tr Q9ERI5	Ptdsr	Phosphatidylserine receptor
1765588	tr Q96F13	Plscr3	Phospholipid scramblase 3
2142939	tr Q9DBY2	Ppp1cp	Phosphoprotein phosphatase (EC 3.1.3.16) 1-beta catalytic chain
1540342	tr Q63430	Al481750	PIPPin protein
1436592	D28132	Vipr2	Pituitary adenylate cyclase-activating polypeptide (PACAP)
1862676	tr Q8VDG3	Parn	Poly(A)-specific ribonuclease
2075615	IMAGE:791455	Pck1	Polycystic kidney gene
1744344	LL: 50192	Pmscl2	Polymyositis/scleroderma autoantigen 2, has exonuclease
2308907	IMAGE:960230	Spop1	POZ 56 protein
1902592	sp Q9M4C4	Pfdn2	Prefoldin subunit 4
1644107	tr Q9JJX1	Cymp	Prothymosin precursor (EC 3.4.23.4)
1476573	tr Q99JZ1	Prlr	Prolactin receptor
1542413	pir JC7083	Prkcbp	protein kinase (EC 2.7.1.37) N beta
1672875	IMAGE:537146	Prkdc	Protein Kinase DNA activating subunit
1796404	sp Q99KW3	TarA	Protein Tara
2232491	sp P14238	Fes	Proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112)
1316383	RHUM090854	Pkwa	Putative serine/threonine-protein kinase pkwa (EC 2.7.1.-)
2199927	tn AAM48241	Pycr1	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)
1554726	sp P50398	Gdi1	RAB GDP dissociation inhibitor alpha
2284221	tr Q9D1P3	Rab25	RAB25, member RAS oncogene family
2071849	tr Q8WU62	Reps1	RALBP1 associated Eps domain containing 1
2291726	tr Q924Z6	2610005L19Rik	RANBP20
2187647	sp Q9JKF1	Iqgap1	Ras GTPase-activating-like protein IQGAP1
1767997	tr Q96QU0	Sara	RasGAP-activating-like protein 2
1474741	sp Q9NRR4	Rib1	Ribonuclease III (EC 3.1.26.3)
1426774	pirnr NF00075137	Rp929	Ribonuclease P protein subunit p29
1808466	tr Q9CQ16	Rpl27a	Ribosomal protein L27a
1541068	tr Q9D77	Mrpl2	Ribosomal protein, mitochondrial, L14
1309316	RFUG18763	Rmil	RMIL serine/threonine-protein kinase (EC 2.7.1.37)
2186858	pirnr NF00512849	Tceb1l	RNA Polymerase II transcription factor SIII subunit
2075437	tr Q9Z118	Neurod1	Rod1
1316119	sp Q9HCY8	S100a15	S100 calcium-binding protein A15
1446182	RHUM230020	Amd1	S-adenosyl methyltransferase
1542150	tr Q9UL12	Sardh	Sarcosine dehydrogenase (EC 1.5.99.1)

2049793	IMAGE:750283	Chi313	Secretory protein precursor (Ym1)
1287847	sp Q9H3S1	Sema4a	Semaphorin 4A precursor
1862318	IMAGE:680284	Sema4g	Semaphorin subclass 4 member G
1446873	pirnr NF00115841	3-Sep	Septin 3; GTPases
1659713	tr Q8VCH3	Serpina3n	Serine protease inhibitor 2; clade A (alpha-1 antiprotease, antitrypsin) 3N
1908006	NM_001626	Ak2	Serine threonine protein kinase, viral oncogene
2186532	tr Q96SU3	Mrbp	Serine/threonine protein kinase PKPA (EC 2.7.1.-)
1649379	RFU026194	BC011468	Serine/threonine protein kinases
2164199	RMU017874	Rad53	Serine/threonine-protein kinase Chk2 (EC 2.7.1.-)
1908636	RCF00521	Alb1	Serum albumin: Afamin
2049985	sp P02739	Saa	Serum amyloid A-2 protein precursor
2235239	tr Q9JHL4	Dbl1	SH3P7R1: debris
2057851	tr Q9EQL9	Sharpin	Sharpin; shank interacting protein
1908569	pirnr NF00048897	Skiip	SKI interacting protein
1325565	sp P43330	Snrpd2	Small nuclear ribonucleoprotein Sm D2
1644037	tr Q91WX6	Snrk	SNF-1 related kinase
2201454	tr Q8VBW1	Creat	Sodium and chloride dependent creatine transporter
1391034	sp Q9NRY64	Slc2a8	Solute carrier family 2, facilitated glucose transporter, member 8
1649568	tr Q8WUG9	Snx12	Sorting nexin 12
1285920	sp Q9D8U8	Snx5	Sorting nexin 5
2073633	tr Q90WG1	Spin	Spindlin
1675453	sp Q99NB9	Sf3b1	Splicing factor 3B subunit 1
1861831	tr Q9XFA1	Spp30	SPP30
1794458	tn AAH28823	Sart1	Squamous cell carcinoma antigen recognized by T-cells 1
1875865	IMAGE:679704	Shc1	Src homology 2 domain-containing transforming protein C1
1937187	tr Q8WXF0	Nssr	SRRP35 - splicing
1905127	tr Q96A24	Biklk	SSX2 interacting protein hRabin3A, isoform beta2
1676097	tr Q9WU4	Stk2	Ste20-related kinase SMAK
1662193	pirnr NF00503126	Mln64-pending	Steroidogenic acute regulatory protein
1861959	RRN04135	1300013A03Rik	Sterol 26-Hydroxylase, mitochondrial precursor (EC 1.14.-.-)
1875374	IMAGE:679322	Stra13	Stra13
1554874	IMAGE:483019	Sep1	Strand exchange protein
1287118	sp Q9W6S3	Mknk1	Stress-activated map kinase interacting protein 1: Mknk1
1752493	sp P11609	Cd1d1	T-cell surface glycoprotein CD1d1 precursor
1494921	IMAGE:458261	Tebp	Telomerase binding protein, p23
1650417	RHS22506	Slc22a1l	Tetracycline transporter-like protein
2158359	tr Q62439	Slc12a3	Thiazide-sensitive Na-Cl cotransporter
1937851	tr Q96P17	Nssr	TLS-associated protein TASR-2
2042203	IMAGE:570489	Tde1l	TMS-2 mRNA

1309228	IMAGE:348928	Tasp	Toll-associated serine protease
1793885	trIQ8R1J9	Tor2a	Torsin family 2, member A
2292059	spIQ9EQS0	Taldo1	Transaldolase (EC 2.2.1.2)
1861530	pirnr NF00397895	Tcea1	transcription elongation factor TFIIIS
1861530	pirnr NF00397895	Tcea2	Transcription elongation factor TFIIIS.oB
1538938	trIQ99L72	Tcfap2c	Transcription factor AP-2, gamma
1752241	trIQ921Z4	Zfp162	Transcription factor ZFM1
1677308	RHUM023513	Tbp	Transcription initiation factor TFIID subunit
1660257	spIP38152	Slc25a1	Tricarboxylate transport protein
1908150	IMAGE:736011	Trim32	Tripartite motif-containing 32; Ubiquitin reactions
1937837	IMAGE:600545	Tulp4	Tubby super-family protein
1903941	RHUM221204	Mid1	Tubulin--tyrosine ligase (EC 6.3.2.25)
1487322	trIQ9TTJ0	Jak2	Tyrosine-protein kinase JAK2 (EC 2.7.1.112)
1553927	pirnr NF00522414	Snrp70	U1 Small nuclear ribonucleoprotein 70 kd
1284184	spIQ9Y4Y8	1500031N17Rik	U6 snRNA-associated Sm-like protein LSM6
2164616	tn AAH27499	Lsm7	U6 snRNA-associated Sm-like protein LSM7
1793047	RHUM015543	Usp18	Ubiquitin carboxyl-terminal hydrolase (EC 3.1.2.15)
2257369	trIQ9H9C5	Usp18	Ubiquitin carboxyl-terminal hydrolase (EC 3.1.2.15)
1895437	RHUM033519	Usp18	Ubiquitin carboxyl-terminal hydrolase 4 (EC 3.1.2.15)
1543807	trIQ8VCW4	Unc93b	unc93 homolog B
1554068	trIQ91VK9	Vps45	Vacuolar protein sorting 45
2187159	spIP16612	Vegfa	Vascular endothelial growth factor-3; VEGF-3
1447666	trIQ96ST6	Vav2	VAV2 protein
1476080	IMAGE:443046	Vat1	Vesicle amine transport protein 1 homolog
2102226	trIQ91YD6	Vilp	Villin-like protein
2262509	IMAGE:904738	Vdac2	Voltage dependent ion channel 2
1896487	IMAGE:746432	Wee1	Wee1 tyrosine kinase
1427891	IMAGE:422959	Foxn1	Whn gene = forkhead box n
1436657	IMAGE:425757	Wbscr5	Williams-Beuren Syndrome gene
1355012	IMAGE:367785	Wrch1	WNT1-responsive CDC46 analog
2073725	IMAGE:778557	Zfp393	Zinc finger protein (Gzf)
2283540	trIQ8VDT8	Pdcd2	Zinc finger protein 189
1464723	spIQ03164	Slc25a17	Zinc finger protein HRX
2076192	trIQ923T4	Zfp358	Zinc finger protein ZFEND
1649248	RHUM020972	Agtpbp1	Zinc-carboxypeptidase precursor (EC 3.4.17.-)
2259460	trIQ8R482	Snai2	Zinc-finger transcription factor SLUG

^a Genes regulated by diet but only in certain genotypes. These reflect genotype X diet interactions.

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FIG 3. GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:**
GI_#:
Chr:
CM:
QTL_Name:
QTL Description:
Gene Function

Mendelian inheritance in Man information and number
GenoInfo number (Genbank identifier)
Chromosome number in mouse
Centimorgan position in mouse
Name of QTL
Describes QTL
QTLs that are +/- 10cM.
Based upon a variety of databases

**GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS
MAPPING TO CHROMOSOME 1 QTLs**

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Hepatic glutaminase (EC 3.5.1.2)	1811443	1	25.9		
(no disease association)					
Linked to diet-induced disease model		1	25	Wt10q1	body weight, 10 weeks, QTL 1
		1	27	Wt6q1	body weight, 6 weeks, QTL 1
		1	21	Dbsty1	diabesity 1
		1	28.7	Obq7	obesity QTL 7
		1	32.8	Hins	hyperinsulinemia
		1	36	Insq2	insulin QTL 2
		1	36	Bw5	body weight QTL 5

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Splicing factor 3B subunit 1 (no disease association)	1675453	1	28.9		
<i>Linked to diet-induced disease model</i>		1	25	Wt10q1	body weight, 10 weeks, QTL 1
		1	27	Wt6q1	body weight, 6 weeks, QTL 1
		1	21	Dbsy1	diabesity 1
		1	28.7	Obq7	obesity QTL 7
		1	32.8	Hins	hyperinsulinemia
		1	36	Insq2	insulin QTL 2
		1	36	Bw5	body weight QTL 5

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Fibronectin	2256866	1	36.1		
Fibronectin glomerulopathy (MIM:601894); Platelet dysfunction (MIM: 225310)					
<i>Linked to diet-induced disease model</i>		1	27	Wt6q1	body weight, 6 weeks, QTL 1
		1	28.7	Obq7	obesity QTL 7
		1	32.8	Hins	hyperinsulinemia
		1	36	Insq2	insulin QTL 2
		1	36	Bw5	body weight QTL 5

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Nucleolin	1355494	1	48.7		
Facioscapulohumeral muscular dystrophy (MIM:158900), possible Multiple endocrine neoplasia, type IIA (MIM:171400)					
<i>Linked to diet-induced disease model</i>		1	41	Bglq1	body growth late QTL 1
		1	41	Sk11	skeletal size (tail length) 1
		1	54.3	Bwtq1	body weight QTL 1
		1	58	Bgeq1	body growth early QTL 1

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Glucuronosyltransferase (EC 2.4.1.17)	1861211	1	51.7		
Hyperbilirubinemias (MIM:143500, 218800;606784) and neonatal hyperbilirubinemia (MIM: 237900)					
<i>Linked to diet-induced disease model</i>		1	54.3	<i>Bwtq1</i>	<i>body weight QTL 1</i>
		1	58	<i>Bgeq1</i>	<i>body growth early QTL 1</i>
		1	62	<i>Fatq1</i>	<i>percent fat, subcutaneous and gonadal, QTL 1</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Regulator of G protein signaling	1841024	1	78		
Leukemia (MIM:600681)					
<i>Linked to diet-induced disease model</i>		1	77	<i>Nidd6</i>	<i>non-insulin-dependent diabetes mellitus 6</i>
		1	69	<i>Bw17</i>	<i>body weight QTL 17</i>
		1	69.1	<i>Obq8</i>	<i>obesity QTL 8</i>
		1	72	<i>Wt3q1</i>	<i>body weight, 3 weeks, QTL 1</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Immediate early gene	1487422	1	81.5		
Responds to addition of serum (none in quiescent state) (MIM: 607177)					
<i>Linked to diet-induced disease model</i>		1	77	<i>Nidd6</i>	<i>non-insulin-dependent diabetes mellitus 6</i>
		1	69	<i>Bw17</i>	<i>body weight QTL 17</i>
		1	69.1	<i>Obq8</i>	<i>obesity QTL 8</i>
		1	72	<i>Wt3q1</i>	<i>body weight, 3 weeks, QTL 1</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Prefoldin subunit 4	1902592	1	92.6		
(no disease association, subunit 3 associated with Von Hippel-Lindau syndrome, transporter of VHL tumor suppressor gene (MIM:300133))					
<i>Linked to diet-induced disease model</i>		1	87.9	<i>Bmd1</i>	<i>bone mineral density 1</i>
		1	88.4	<i>Obq9</i>	<i>obesity QTL 9</i>
		1	102	<i>Batq1</i>	<i>brown fat QTL 1</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Duffy antigen/receptor for chemokine	1902535	1	94		
CMKBR5 was identified as a coreceptor for the human immunodeficiency virus-1 (HIV-1) (MIM: 601373)					
<i>Linked to diet-induced disease model</i>		1	87.9	<i>Bmd1</i>	<i>bone mineral density 1</i>
		1	88.4	<i>Obq9</i>	<i>obesity QTL 9</i>
		1	102	<i>Batq1</i>	<i>brown fat QTL 1</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
F11r	1446049	1	93.5		
Ligand for the integrin LFA1; a platelet receptor (MIM: 605721)					
<i>Linked to diet-induced disease model</i>		1	87.9	<i>Bmd1</i>	<i>bone mineral density 1</i>
		1	88.4	<i>Obq9</i>	<i>obesity QTL 9</i>
		1	102	<i>Batq1</i>	<i>brown fat QTL 1</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
E1-E2 subunit of ATPase, membrane	1446049	1	94		
Atp1A4 no disease link (MIM: 607321)					
<i>Linked to diet-induced disease model</i>		1	87.9	<i>Bmd1</i>	<i>bone mineral density 1</i>
		1	88.4	<i>Obq9</i>	<i>obesity QTL 9</i>
		1	102	<i>Batq1</i>	<i>brown fat QTL 1</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 2 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:**
GI_#:
Chr:
CM:
QTL_Name:
QTL_Description:
Gene Function

Mendelian inheritance in Man information and number
GenoInfo number (Genbank identifier)
Chromosome number in mouse
Centimorgan position in mouse
Name of QTL
Describes QTL
QTLs that are +/- 10cM.
Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
VAV2 oncogene	1447666	2	15.3		
Oncogene					
<i>Linked to diet-induced disease model</i>		2	5	Diet1	<i>variability in response to cholesterol atherogenic diet</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Adenylate kinase, cytosolic	2235102	2	21.6		
Hemolytic anemia, involved in energy metabolism (MIM: 103000)					
<i>Linked to diet-induced disease model</i>		2	31	Wg1	<i>weight gain in high growth mice 1</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Gelsolin	2102585	2	24		
CMKBR5 was identified as a coreceptor for the human immunodeficiency virus-1 (HIV-1) (MIM: 601373)					
<i>Linked to diet-induced disease model</i>		2	31	<i>Wg1</i>	<i>weight gain in high growth mice 1</i>
		2	34.5	<i>Nidd5</i>	<i>non-insulin-dependent diabetes mellitus 5</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Solute carrier family 2, facilitated glucose transporter 8	1391034	2	24		
Glut2 is associated with Fanconi Bickel syndrome (MIM: 227810),hepatorenal glycogen accumulation. #8 not described yet					
<i>Linked to diet-induced disease model</i>		2	31	<i>Wg1</i>	<i>weight gain in high growth mice 1</i>
		2	34.5	<i>Nidd5</i>	<i>non-insulin-dependent diabetes mellitus 5</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
CD59A	2248057	2	55		
Protectin, prevents complement activated cell killing (MIM: 107271)					
<i>Linked to diet-induced disease model</i>		2	53	<i>Obq3</i>	<i>obesity QTL 3</i>
		2	56	<i>Bw6</i>	<i>body weight QTL 6</i>
		2	49.6	<i>Mob6</i>	<i>multigenic obesity 6</i>
		2	58.1	<i>Obq10</i>	<i>obesity QTL 10</i>
		2	61	<i>Bwfq1</i>	<i>body weight and fat QTL 1</i>
		2	61	<i>Wg2</i>	<i>weight gain in high growth mice 2</i>
		2	63	<i>Cara1</i>	<i>carcass ash in high growth mice 1</i>
		2	63	<i>Carp1</i>	<i>carcass protein in high growth mice 1</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
HECT Ubiquitin protein ligase E3 (EC 6.3.2.-)	1464733	2	67.4		
Protectin, prevents complement activated cell killing (MIM: 107271)					
<i>Linked to diet-induced disease model</i>		2	69	<i>Bgeq2</i>	<i>body growth early QTL 2</i>
		2	58.1	<i>Obq10</i>	<i>obesity QTL 10</i>
		2	61	<i>Bwfq1</i>	<i>body weight and fat QTL 1</i>
		2	61	<i>Wg2</i>	<i>weight gain in high growth mice 2</i>
		2	63	<i>Cara1</i>	<i>carcass ash in high growth mice 1</i>
		2	71	<i>Hlq2</i>	<i>heat loss QTL 2</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
GA-binding protein transcription factor, beta subunit 1	1487297	2	71		
Regulates mitochondrial gene expression in nucleus (MIM: 604408)					
<i>Linked to diet-induced disease model</i>		2	71	<i>Hlq2</i>	<i>heat loss QTL 2</i>
		2	81	<i>Bfq1</i>	<i>body fat QTL 1</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Histidine decarboxylase (EC 4.1.1.22)	1487297	2	71		
neurotransmission, gastric acid secretion, and smooth muscle tone (MIM: 142704)					
<i>Linked to diet-induced disease model</i>		2	71	<i>Hlq2</i>	<i>heat loss QTL 2</i>
		2	81	<i>Bfq1</i>	<i>body fat QTL 1</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Attractin	1556028	2	73.9		
Mouse mahogany gene, control of pigmentation and energy metabolism (body weight in brain), low affinity acceptor of Agouti (MIM: 603130)					
<i>Linked to diet-induced disease model</i>		2	71	<i>Hlq2</i>	<i>heat loss QTL 2</i>
		2	69	<i>Bgeq2</i>	<i>body growth early QTL 2</i>
		2	81	<i>Bfq1</i>	<i>body fat QTL 1</i>
		2	84	<i>Bglq2</i>	<i>body growth late QTL 2</i>
		2	84	<i>Bwfg2</i>	<i>body weight and fat QTL 2</i>
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Glycogen phosphorylase (EC 2.4.1.1)	1355364	2	84		
Glycogen storage disease in muscle (MIM: 232600)					
<i>Linked to diet-induced disease model</i>		2	83	<i>Bts1</i>	<i>bladder tumor susceptibility 1</i>
		2	84	<i>Bglq2</i>	<i>body growth late QTL 2</i>
		2	84	<i>Bwfg2</i>	<i>body weight and fat QTL 2</i>
		2	84.2	<i>Bdt1</i>	<i>bone density traits 1</i>
		2	81	<i>Bfq1</i>	<i>body fat QTL 1</i>
		2	87	<i>Bglu1</i>	<i>blood glucose level 1</i>
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Tcea2 transcription elongation factor TFIIIS	1861530	2	103.1		
No disease association (MIM: 604784)					
<i>Linked to diet-induced disease model</i>		2	95.5	<i>Mob5</i>	<i>multigenic obesity 5</i>
		2	99	<i>Hcs4</i>	<i>hepatocarcinogenesis susceptibility 4</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 3 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:** Mendelian inheritance in Man information and number
- GI_#:** GenoInfo number (Genbank identifier)
- Chr:** Chromosome number in mouse
- CM:** Centimorgan position in mouse
- QTL_Name:** Name of QTL
- QTL_Description:** Describes QTL
- Gene Function:** QTLs that are +/- 10cM. Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Neprilysin-like peptidase gamma	2271912	3	29.6		
Alzheimer's, a candidate amyloid-beta-degrading peptidase (MIM: 104300)					
<i>Linked to diet-induced disease model</i>		3	22	<i>Idd3</i>	<i>Insulin dependent diabetes</i>
		3	30	<i>Afw1</i>	<i>abdominal fat weight QTL 1</i>
		3	26	<i>Afpq1</i>	<i>abdominal fat percent QTL 1</i>
		3	35	<i>Hlq3</i>	<i>heat loss QTL 3</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Interleukin 6 receptor, alpha	1889604	3	42.1		
Immune response, hematopoiesis, and acute-phase reactions (MIM: 147880)					
<i>Linked to diet-induced disease model</i>		3	35	<i>Hlq3</i>	<i>heat loss QTL 3</i>
		3	49	<i>Bglq3</i>	<i>body growth late QTL 3</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Cathepsin S	1310123	3	42.7		
MHC class II haplotype and Ctss activity are regulators of NK T cells (116845)					
<i>Linked to diet-induced disease model</i>		3	35	Hlq3	heat loss QTL 3
		3	49	Bglq3	body growth late QTL 3
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Shc transforming protein (Shc1)	1875865	3	45.0		
May regulate stress apoptotic responses and life span in mammals (MIM: 600560)					
<i>Linked to diet-induced disease model</i>		3	35	Hlq3	heat loss QTL 3
		3	49	Bglq3	body growth late QTL 3
		3	55	Batq2	brown fat QTL 2
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5)	1497254	3	48		
Alzheimer's, a candidate amyloid-beta-degrading peptidase (MIM: 142940)					
<i>Linked to diet-induced disease model</i>		3	55	Batq2	brown fat QTL 2
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
T-cell surface glycoprotein CD1d1	1752493	3	48		
Natural killer (NK) T cell, active in autoimmune diabetes, tumor rejection, and some microbial infections (MIM: 188410)					
<i>Linked to diet-induced disease model</i>		3	55	Batq2	brown fat QTL 2

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
N-ras	1290045	3	48		
Oncogene (PMID: 2835730)					
<i>Linked to diet-induced disease model</i>		3	55	Batq2	brown fat QTL 2
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Vacuolar protein sorting 45	1554068	3	50		
trafficking of proteins between the trans-Golgi network and the lysosome (MIM: 606045)					
<i>Linked to diet-induced disease model</i>		3	49	Bglq3	body growth late QTL 3
		3	55	Batq2	brown fat QTL 2
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Chitinase (Chi313)	2049793	3	50.5		
May be involved in hematopoiesis and inflammation (PMID: 12101265)					
<i>Linked to diet-induced disease model</i>		3	49	Bglq3	body growth late QTL 3
		3	55	Batq2	brown fat QTL 2
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
ATP synthase beta chain (EC 3.6.3.14)	1655040	3	57		
Energy metabolism, ATP formation (MIM: 102910)					
<i>Linked to diet-induced disease model</i>		3	55	Batq2	brown fat QTL 2
		3	49	Bglq3	body growth late QTL 3
		3	61	Wt10q2	body weight, 10 weeks, QTL 2

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Guanylate binding protein 2	1751874	3	67.4		
Uterine receptivity ? (MIM: 600412)					
<i>Linked to diet-induced disease model</i>		3	64.1	<i>Bdt2</i>	<i>bone density traits 2</i>
		3	61	<i>Wt10q2</i>	<i>body weight, 10 weeks, QTL 2</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 4 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

MIM: Mendelian inheritance in Man information and number
GI_#: GenInfo number (Genbank identifier)
Chr: Chromosome number in mouse
CM: Centimorgan position in mouse
QTL_Name: Name of QTL
QTL Description: Describes QTL
Gene Function: QTLs that are +/- 10cM.
Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Cytochrome P450 Cyp4a	1555555	4	49.5		
Higher expression in bladder cancer than normal bladder (MIM: 124075)					
<i>Linked to diet-induced disease model</i>		4	42.5	<i>Bgeq3</i>	<i>body growth early QTL 3</i>
		4	55	<i>Bwtq2</i>	<i>body weight QTL 2</i>
		4	59	<i>Bw7</i>	<i>body weight QTL 7</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 5 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:** Mendelian inheritance in Man information and number
- GI_#:** GenolInfo number (Genbank identifier)
- Chr:** Chromosome number in mouse
- CM:** Centimorgan position in mouse
- QTL_Name:** Name of QTL
- QTL_Description:** Describes QTL
- Gene Function:** QTLs that are +/- 10cM. Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Replication factor C large subunit	1318639	5	39		
Linked to diet-induced disease model		5	38	Carf1	carcass fat in high growth mice 1
		5	29	Obq12	obesity QTL 12
		5	42	Bw8	body weight QTL 8
		5	44	Bwob	body weight of obese males
		5	45	Dbsty2	diabesity 2

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Serum albumin (afamin)	1908636	5	50		
Linked to diet-induced disease model		5	51	Afpq3	abdominal fat percent QTL 3
		5	42	Bw8	body weight QTL 8
		5	44	Bwob	body weight of obese males
		5	45	Dbsty2	diabesity 2
		5	54	Bwem1	body weight day 30 males 1

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Huntingtin interacting protein 1	1283303	5	75		
Similar to Sla2p, a protein essential for function of the cytoskeleton in <i>S. cerevisiae</i> . (MIM: 601767)					
<i>Linked to diet-induced disease model</i>		5	70	<i>Bwefm</i>	<i>body weight females and males day 10</i>
		5	78	<i>Bglq14</i>	<i>body growth late QTL 14</i>
		5	80	<i>Afw3</i>	<i>abdominal fat weight QTL 3</i>
		5	81	<i>Bw13</i>	<i>body weight QTL 13</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 6 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

MIM: Mendelian inheritance in Man information and number
GI_#: GenInfo number (Genbank identifier)
Chr: Chromosome number in mouse
CM: Centimorgan position in mouse
QTL_Name: Name of QTL
QTL Description: Describes QTL
Gene Function QTLs that are +/- 10cM.
Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Aquaporin 1	1752249	6	27		
Water transport (MIM: 107776)					
<i>Linked to diet-induced disease model</i>		6	26.8	<i>Obq13</i>	<i>obesity QTL 13</i>
		6	35	<i>Bw18</i>	<i>body weight QTL 18</i>
		6	35.5	<i>Nidd3n</i>	<i>non-insulin-dependent diabetes mellitus 3 in NSY</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Ubiquitin carboxyl-terminal hydrolase	1793047 1895437 2157776	6	56	2 copies of (EC 3.1.2.15) and 1 of (EC.3.4.19.12)	
Candidate gene for Parkinson's Syndrome (MIM: 191342)					
<i>Linked to diet-induced disease model</i>		6	46.3	<i>Adip2</i>	<i>adiposity 2</i>
		6	46.3	<i>Bgeq4</i>	<i>body growth early QTL 4</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Alpha-2-macroglobulin	2042386	6	62		
Candidate gene for Parkinson's Syndrome (MIM: 103942)					
<i>Linked to diet-induced disease model</i>		6	67	<i>Bdt3</i>	<i>bone density traits 3</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Transforming protein c-Ki-ras-1, hepatic	1915216	6	56	2 copies of (EC 3.1.2.15) and 1 of (EC.3.4.19.12)	
Mutated in many cancers, p21 (MIM: 190070)					
<i>Linked to diet-induced disease model</i>		6	67	<i>Bdt3</i>	<i>bone density traits 3</i>
		6	74	<i>Bglq5</i>	<i>body growth late QTL 5</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 7 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:** Mendelian inheritance in Man information and number
- GI_#:** GenInfo number (Genbank identifier)
- Chr:** Chromosome number in mouse
- CM:** Centimorgan position in mouse
- QTL_Name:** Name of QTL
- QTL_Description:** Describes QTL QTLs that are +/- 10cM.
- Gene Function** Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Testosterone regulated RP2	1715326	7	15		
Hypothetical protein – no OMIM					
<i>Linked to diet-induced disease model</i>		7	22	<i>Afpq9</i>	<i>abdominal fat percent QTL 9</i>
		7	23	<i>Afw9</i>	<i>abdominal fat weight QTL 9</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
G1/S-specific cyclin E1	1746733	7	16		
More expression, more severe breast cancer (MIM: 123837)					
<i>Linked to diet-induced disease model</i>		7	22	<i>Afpq9</i>	<i>abdominal fat percent QTL 9</i>
		7	23	<i>Afw9</i>	<i>abdominal fat weight QTL 9</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
U1 Small ribonucleoprotein 70kd	1553927	7	23		
Splicing of mRNA (MIM: 180740)					
<i>Linked to diet-induced disease model</i>		7	22	<i>Afpq9</i>	<i>abdominal fat percent QTL 9</i>
		7	23	<i>Afw9</i>	<i>abdominal fat weight QTL 9</i>
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Serum amyloid A-2 protein	2049985	7	23.5		
From amyloid precursor protein (APP) involved in Alzheimer's (MIM: 104761)					
<i>Linked to diet-induced disease model</i>		7	22	<i>Afpq9</i>	<i>abdominal fat percent QTL 9</i>
		7	23	<i>Afw9</i>	<i>abdominal fat weight QTL 9</i>
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Ras GTPase-activating-like protein IQGAP1	2187647	7	39		
Motifs in protein modulates calmodulin binding and co-localizes with actin, cell morphology (MIM: 603379)					
<i>Linked to diet-induced disease model</i>		7	30	<i>Bgeq5</i>	<i>body growth early QTL 5</i>
		7	46.6	<i>Adip3</i>	<i>adiposity 3</i>
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Ribosomal protein L27a	1808466	7	51.5		
Ribosomal protein (MIM: 603637)					
<i>Linked to diet-induced disease model</i>		7	50	<i>Bglq6</i>	<i>body growth late QTL 6</i>
		7	51.4	<i>Obq15</i>	<i>obesity QTL 15</i>
		7	46.6	<i>Adip3</i>	<i>adiposity 3</i>
		7	61	<i>Hlq5</i>	<i>heat loss QTL 5</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Coatomer beta subunit	1497811	7	53.3		
Involved in golgi and secretory traffic (MIM: 600959)					
<i>Linked to diet-induced disease model</i>		7	51.4	Obq15	obesity QTL 15
		7	46.6	Adip3	adiposity 3
		7	50	Bglq6	body growth late QTL 6
		7	61	Hlq5	heat loss QTL 5
		7	62	Mob1	multigenic obesity 1

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
CLN3 protein	1676738	7	64		
Neurodegenerative disorders, accumulates lipopigment, phospholipase A1 deficiency (MIM: 204200)					
<i>Linked to diet-induced disease model</i>		7	62	Mob1	multigenic obesity 1
		7	61	Hlq5	heat loss QTL 5
		7	70	Bgeq6	body growth early QTL 6

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Tetracycline transporter-like protein	1650417	7	65.5		
Organic cation transporter, found mutated in several neoplasias (including breast) (MIM: 602631)					
<i>Linked to diet-induced disease model</i>		7	61	Hlq5	heat loss QTL 5
		7	62	Mob1	multigenic obesity 1
		7	70	Bgeq6	body growth early QTL 6
		7	70	Bgeq6	body growth early QTL 6

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Alcohol dehydrogenase [NADP+] (EC 1.1.1.2); Aldr3	1700965	7	68		
Aldose reductase. In diabetic hyperglycemia, significant quantities of sorbitol produced, cause neuropathy, retinopathy, and cataracts (MIM: 103880)					
<i>Linked to diet-induced disease model</i>		7	70	<i>Bgeq6</i>	<i>body growth early QTL 6</i>
		7	61	<i>Hlq5</i>	<i>heat loss QTL 5</i>
		7	62	<i>Mob1</i>	<i>multigenic obesity 1</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 8 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

MIM: Mendelian inheritance in Man information and number
GI_#: GenInfo number (Genbank identifier)
Chr: Chromosome number in mouse
CM: Centimorgan position in mouse
QTL_Name: Name of QTL
QTL Description: Describes QTL
Gene Function QTLs that are +/- 10cM.
Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Liver carboxylesterase 22 (EC 3.1.1.1)	1861663	8	43		
Detoxification of foreign compounds (MIM: 114835)					
<i>Linked to diet-induced disease model</i>		8	45	<i>Wg3</i>	<i>weight gain in high growth mice 3</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Thiazide-sensitive Na-Cl cotransporter	2158359	8	45		
Na+/Cl- transporter (MIM: 600948)					
<i>Linked to diet-induced disease model</i>		8	45	<i>Wg3</i>	<i>weight gain in high growth mice 3</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 9 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:** Mendelian inheritance in Man information and number
- GI_#:** GenInfo number (Genbank identifier)
- Chr:** Chromosome number in mouse
- CM:** Centimorgan position in mouse
- QTL_Name:** Name of QTL
- QTL Description:** Describes QTL
- Gene Function:** QTLs that are +/- 10cM.
Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37)	1497664	9	5		
DNA methylation is altered in many neoplasias (MIM: 126375)					
<i>Linked to diet-induced disease model</i>		9	8	<i>Bwtq4</i>	<i>body weight QTL 4</i>
		9	10	<i>Carf2</i>	<i>carcass fat in high growth mice 2</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Acetyl-Co A acetyltransferase 1, mitochondrial	1539949	9	30		
Mutations may cause ketoacidosis, also found in diabetes (MIM: 607809)					
<i>Linked to diet-induced disease model</i>		9	29	<i>Afw4</i>	abdominal fat weight QTL 4

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Myosin Va	1660028	9	42		
Pigmentary dilution, variable cellular immunodeficiency, and acute phases of uncontrolled lymphocyte and macrophage activation (MIM: 160777)					
<i>Linked to diet-induced disease model</i>		9	42	<i>Adip5</i>	<i>adiposity 5</i>
		9	42	<i>Mob8</i>	<i>multigenic obesity 8</i>
		9	48	<i>Bglq7</i>	<i>body growth late QTL 7</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Rbp1 Deleted in split hand/split foot protein 1	2187287	9	52		
Retinol binding protein – Vitamin A alcohol transporter (MIM: 180260)					
<i>Linked to diet-induced disease model</i>		9	42	<i>Adip5</i>	<i>adiposity 5</i>
		9	42	<i>Mob8</i>	<i>multigenic obesity 8</i>
		9	48	<i>Bglq7</i>	<i>body growth late QTL 7</i>
		9	60	<i>Dob2</i>	<i>dietary obesity 2</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Laminin, beta 2	1509303	9	60		
Important for cell differentiation, adhesion, migration, and neurite outgrowth (MIM: 150325)					
<i>Linked to diet-induced disease model</i>		9	60	<i>Dob2</i>	<i>dietary obesity 2</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 10 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:**
GI_#:
Chr:
CM:
QTL_Name:
QTL_Description:
Gene Function

Mendelian inheritance in Man information and number
GenoInfo number (Genbank identifier)
Chromosome number in mouse
Centimorgan position in mouse
Name of QTL
Describes QTL
QTLs that are +/- 10cM.
Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Cabin1, Calcineurin inhibitor	2164107	10	40.7		
CABIN1 recruits mSIN3 and its associated histone deacetylases, histone acetylation controls transcription processes (MIM: 604251)					
<i>Linked to diet-induced disease model</i>		10	46	<i>Igfbp3q2</i>	<i>insulin-like growth factor binding protein 3 QTL 2</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Metalloproteinase inhibitor 3 precursor	2041342	10	47		
Sorsby fundus dystrophy, central (macular) lesion showing edema, hemorrhage, and exudates (MIM: 188826)					
<i>Linked to diet-induced disease model</i>		10	57	<i>Bgeq8</i>	<i>body growth early QTL 8</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Histidine ammonia-lyase (EC 4.3.1.3); histidase	1895338	10	51		
Histidinemia is a benign metabolic disorder that does not require treatment (MIM: 235800)					
<i>Linked to diet-induced disease model</i>					
		10	57	Bgeq8	body growth early QTL 8
		10	59	Insq4	insulin QTL 4
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
C2H2 zinc finger transcription factor JING	2075615	10	69		
Glioma-associated oncogene (GLI) involved in basal cell carcinomas (MIM: 165220)					
<i>Linked to diet-induced disease model</i>		10	59	Insq4	insulin QTL 4
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
DNA helicase	2308561	10	69		
DNA replication (MIM: 165220)					
<i>Linked to diet-induced disease model</i>		10	59	Insq4	insulin QTL 4

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 11 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:** Mendelian inheritance in Man information and number
- GI_#:** GenolInfo number (Genbank identifier)
- Chr:** Chromosome number in mouse
- CM:** Centimorgan position in mouse
- QTL_Name:** Name of QTL
- QTL_Description:** Describes QTL
- Gene Function:** QTLs that are +/- 10cM. Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
MCAMK1-BETA2	1282018	11	0.5		
Calcium/calmodulin-dependent protein kinase (CaM kinase) II beta (CAMK2B) (no MIM)					
<i>Linked to diet-induced disease model</i>		11	1.5	<i>Bglq8</i>	<i>body growth late QTL 8</i>
		11	2	<i>Nidd4n</i>	<i>non-insulin-dependent diabetes mellitus 4 in NSY</i>
		11	9	<i>Afpq5</i>	<i>abdominal fat percent QTL 5</i>
		11	10	<i>Afw5</i>	<i>abdominal fat weight QTL 5</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
SH3P7R1 Debrin	2235239	11	1		
Monoxygenase ? (No MIM)					
<i>Linked to diet-induced disease model</i>		11	1.5	<i>Bglq8</i>	<i>body growth late QTL 8</i>
		11	2	<i>Nidd4n</i>	<i>non-insulin-dependent diabetes mellitus 4 in NSY</i>
		11	9	<i>Afpq5</i>	<i>abdominal fat percent QTL 5</i>
		11	10	<i>Afw5</i>	<i>abdominal fat weight QTL 5</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Hemoglobin alpha chain	1514269	11	16		
Thalassemias (MIM: 141800)					
<i>Linked to diet-induced disease model</i>		11	14	Bw16	body weight QTL 16
		11	9	Afpq5	abdominal fat percent QTL 5
		11	10	Afw5	abdominal fat weight QTL 5
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
SNF-1 related kinase	1644037	11	22		
Protein serine/threonine kinase (MIM: 605705)					
<i>Linked to diet-induced disease model</i>		11	14	Bw16	body weight QTL 16
		11	27.8	Bwtq5	body weight QTL 5
		11	31	Nidd1n	non-insulin-dependent diabetes mellitus 1 in NSY
		11	32	Wt10q3	body weight, 10 weeks, QTL 3
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
RNA Polymerase II, SIII subunit	2186858	11	31		
Transcription factor (MIM: 600695)					
<i>Linked to diet-induced disease model</i>		11	31	Nidd1n	non-insulin-dependent diabetes mellitus 1 in NSY
		11	32	Wt10q3	body weight, 10 weeks, QTL 3
		11	27.8	Bwtq5	body weight QTL 5
		11	36	Wt6q3	body weight, 6 weeks, QTL 3
		11	40	Bgeq9	body growth early QTL 9

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Acidic 82 kDa protein	1650569	11	37		
Complement component C1q binding protein (MIM: 610269)					
<i>Linked to diet-induced disease model</i>		11	36	Wt6q3	body weight, 6 weeks, QTL 3
		11	27.8	Bwtq5	body weight QTL 5
		11	31	Nidd1n	non-insulin-dependent diabetes mellitus 1 in NSY
		11	32	Wt10q3	body weight, 10 weeks, QTL 3
		11	46	Wg4	weight gain in high growth mice 4

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Sperm associated antigen 7	1355309	11	42		
Single stranded DNA binding protein – locus link entry					
<i>Linked to diet-induced disease model</i>		11	36	Wt6q3	body weight, 6 weeks, QTL 3
		11	27.8	Bwtq5	body weight QTL 5
		11	31	Nidd1n	non-insulin-dependent diabetes mellitus 1 in NSY
		11	32	Wt10q3	body weight, 10 weeks, QTL 3
		11	46	Wg4	weight gain in high growth mice 4
		11	51.8	Pbd1	peak bone density 1

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Phospholipid scramblase 3	1765588	11	43		
Transfers lipids across leaflet similar to MIM: 604170					
<i>Linked to diet-induced disease model</i>		11	36	Wt6q3	body weight, 6 weeks, QTL 3
		11	27.8	Bwtq5	body weight QTL 5
		11	31	Nidd1n	non-insulin-dependent diabetes mellitus 1 in NSY
		11	32	Wt10q3	body weight, 10 weeks, QTL 3
		11	46	Wg4	weight gain in high growth mice 4
		11	51.8	Pbd1	peak bone density 1

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Foxn1, Forkhead transcription factor	1427891	11	45		
Involved in hair growth and immune function MIM: 600838					
<i>Linked to diet-induced disease model</i>		11	36	Wt6q3	body weight, 6 weeks, QTL 3
		11	46	Wg4	weight gain in high growth mice 4
		11	51.8	Pbd1	peak bone density 1
		11	55	Bw4	body weight QTL 4
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Gamma transducing activity polypeptide 2	1317824	11	57		
GMPase in rod cells (MIM: 189970)					
<i>Linked to diet-induced disease model</i>		11	51.8	Pbd1	peak bone density 1
		11	55	Bw4	body weight QTL 4
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Retinoic acid receptor alpha	1826093	11	57.8		
Retinoic acid is a vitamin A metabolite (MIM:180240)					
<i>Linked to diet-induced disease model</i>		11	51.8	Pbd1	peak bone density 1
		11	55	Bw4	body weight QTL 4
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Gna13	1826093	11	68		
Angiogenesis and regulation of cell movement (MIM:604406)					
<i>Linked to diet-induced disease model</i>		11	68	Nidd4	Non-insulin dependent diabetes mellitus 2
		11	70	Triglg2	Triglyceride QTL 2
		11	77	Bgeg10	Body growth early QTL 10

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Protein disulfide-isomerase (EC 5.3.4.1)	1328575	11	80		
Prolyl 4-hydroxylase Also known as glutathione-insulin transhydrogenase (MIM: 176790)					
<i>Linked to diet-induced disease model</i>		11	77	<i>Bgeq10</i>	<i>body growth early QTL 10</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 12 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

MIM: Mendelian inheritance in Man information and number
GI_#: GenInfo number (Genbank identifier)
Chr: Chromosome number in mouse
CM: Centimorgan position in mouse
QTL_Name: Name of QTL
QTL Description: Describes QTL
 QTLs that are +/- 10cM.
Gene Function Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Odd-skipped related 1 protein	1446725	12	1		
Calcium/calmodulin-dependent protein kinase (CaM kinase) II beta (CAMK2B) (no MIM)					
<i>Linked to diet-induced disease model</i>		12	17	<i>Bw9</i>	<i>body weight QTL 9</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Peroxidasin, Thyroid peroxidase precursor	1427567	12	15		
Thyroid function (MIM: 606765)					
<i>Linked to diet-induced disease model</i>		12	17	Bw9	body weight QTL 9
		12	18	Afpq10	abdominal fat percent QTL 10
		12	21	Afw10	abdominal fat weight QTL 10
		12	22	Bglq9	body growth late QTL 9

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Dihydrolipoamide dehydrogenase (Dld)	1562575	12	15.1		
Lactic acidosis (MIM: 246900)					
<i>Linked to diet-induced disease model</i>		12	17	Bw9	body weight QTL 9
		12	18	Afpq10	abdominal fat percent QTL 10
		12	21	Afw10	abdominal fat weight QTL 10
		12	22	Bglq9	body growth late QTL 9

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
β -spectrin (Spnb-1)	1530059	12	33		
Mutations cause severe hemolytic anemia (PMID: 8219239)					
<i>Linked to diet-induced disease model</i>		12	34	C10bw7	castaneus 10 week body weight 7

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 13 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:** Mendelian inheritance in Man information and number
- GI_#:** GenolInfo number (Genbank identifier)
- Chr:** Chromosome number in mouse
- CM:** Centimorgan position in mouse
- QTL_Name:** Name of QTL
- QTL_Description:** Describes QTL
- Gene Function:** QTLs that are +/- 10cM. Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL_Description
Frizzled-related protein 4	1630486	13	7		
Signaling function of the WNT/frizzled pathway is antagonized by secreted frizzled-related proteins (MIM: 606570)					
<i>Linked to diet-induced disease model</i>		13	8.3	<i>Pbd2</i>	<i>peak bone density 2</i>
		13	10	<i>Bw15</i>	<i>body weight QTL 15</i>
		13	11	<i>Afw6</i>	<i>abdominal fat weight QTL 6</i>
		13	13	<i>Afpq4</i>	<i>abdominal fat percent QTL 4</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL_Description
Serine proteinase inhibitor NK13	1650732	13	16		
Serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SerpinaB6) (MIM: 173321)					
<i>Linked to diet-induced disease model</i>		13	8.3	<i>Pbd2</i>	<i>peak bone density 2</i>
		13	10	<i>Bw15</i>	<i>body weight QTL 15</i>
		13	11	<i>Afw6</i>	<i>abdominal fat weight QTL 6</i>
		13	13	<i>Afpq4</i>	<i>abdominal fat percent QTL 4</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Jumonji	1372685	13	27		
Regulator of cyclin D, involved in neural tube formation (PMID: 12852854)					
<i>Linked to diet-induced disease model</i>		13	34	Bw10	body weight QTL 10
		13	35	Bwem2	body weight day 30 males 2

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Spindlin	2073633	13	31		
Cell cycle regulator (no MIM)					
<i>Linked to diet-induced disease model</i>		13	34	Bw10	body weight QTL 10
		13	35	Bwem2	body weight day 30 males 2

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Zinc-carboxypeptidase precursor (EC 3.4.17.)	1649248	13	31		
Initially cloned from spinal cords (MIM: 606830)					
<i>Linked to diet-induced disease model</i>		13	34	Bw10	body weight QTL 10
		13	35	Bwem2	body weight day 30 males 2
		13	45	Bglq10	body growth late QTL 10

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 14 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:** Mendelian inheritance in Man information and number
- GI_#:** GenInfo number (Genbank identifier)
- Chr:** Chromosome number in mouse
- CM:** Centimorgan position in mouse
- QTL_Name:** Name of QTL
- QTL_Description:** Describes QTL
- Gene Function:** QTLs that are +/- 10cM. Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Ghitm – Growth hormone inducible protein	1913128	14	15		
(No MIM)					
<i>Linked to diet-induced disease model</i>		14	22	<i>Bglq15</i>	<i>body growth late QTL 15</i>
		14	22.5	<i>Bgeq13</i>	<i>body growth early QTL 13</i>
		14	22.5	<i>Nidd2n</i>	<i>non-insulin-dependent diabetes mellitus 2 in NSY</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Ribonuclease III (EC 3.1.26.3)	1474741	14	18.5		
(No MIM)					
<i>Linked to diet-induced disease model</i>		14	22	<i>Bglq15</i>	<i>body growth late QTL 15</i>
		14	22.5	<i>Bgeq13</i>	<i>body growth early QTL 13</i>
		14	22.5	<i>Nidd2n</i>	<i>non-insulin-dependent diabetes mellitus 2 in NSY</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
T-cell receptor	1542473	14	19.5		
Immune response (MIM: 186880)					
<i>Linked to diet-induced disease model</i>		14	22	<i>Bglq15</i>	<i>body growth late QTL 15</i>
		14	22.5	<i>Bgeq13</i>	<i>body growth early QTL 13</i>
		14	22.5	<i>Nidd2n</i>	<i>non-insulin-dependent diabetes mellitus 2 in NSY</i>
Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
2-hydroxymuconic semialdehyde hydrolase (EC 3.7.1.9)	1649287	14	32.5		
Metabolism of polycyclic aromatic hydrocarbons (MIM: 132811)					
<i>Linked to diet-induced disease model</i>		14	22.5	<i>Bgeq13</i>	<i>body growth early QTL 13</i>
		14	22.5	<i>Nidd2n</i>	<i>non-insulin-dependent diabetes mellitus 2 in NSY</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS **MAPPING TO CHROMOSOME 15 QTLs**

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:**
GI_#:
Chr:
CM:
QTL_Name:
QTL_Description:
Gene Function

Mendelian inheritance in Man information and number
GenoInfo number (Genbank identifier)
Chromosome number in mouse
Centimorgan position in mouse
Name of QTL
Describes QTL
QTLs that are +/- 10cM.
Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Prolactin receptor	1476573	15	4.6		
Mammalian reproduction, growth hormone analog (MIM: 176761)					
<i>Linked to diet-induced disease model</i>		15	6	Bw11	body weight QTL 11
		15	6.7	Mob4	multigenic obesity 4
		15	6.7	Bdf5	bone density traits 5
		15	12.3	Dob9	dietary obesity 9
		15	14.2	Yv	yellow value
		15	14.2	Pheo	pheomelanin

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Growth hormone secretagogue receptor 1	1488749	15	4.6		
Regulates release of Growth hormone (MIM: 601898)					
<i>Linked to diet-induced disease model</i>		15	6	Bw11	body weight QTL 11
		15	6.7	Mob4	multigenic obesity 4
		15	6.7	Bdt5	bone density traits 5
		15	12.3	Dob9	dietary obesity 9
		15	14.2	Yv	yellow value
		15	14.2	Pheo	pheomelanin

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
δ - Neurocalcin (NCALD)	1325306	15	11		
Signal transduction (MIM: 606722)					
<i>Linked to diet-induced disease model</i>		15	6	Bw11	body weight QTL 11
		15	6.7	Mob4	multigenic obesity 4
		15	6.7	Bdt5	bone density traits 5
		15	12.3	Dob9	dietary obesity 9
		15	14.2	Yv	yellow value
		15	14.2	Pheo	pheomelanin
		15	18.35	Dob4	dietary obesity 4

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
C-myc protein	2284153	15	32		
Helix-loop-helix transcription factor and oncogene (MIM: 190080)					
<i>Linked to diet-induced disease model</i>		15	22	Bglq16	body growth late QTL 16
		15	22	Bglq16	body growth late QTL 16
		15	22	Bgeq14	body growth early QTL 14
		15	22.8	Dob3	dietary obesity 3
		15	41.2	Bwtq6	body weight QTL 6

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Myosin heavy chain, fast skeletal muscle	1464684	15	43.3		
Hallmark of muscle regeneration (MIM: 160720)					
<i>Linked to diet-induced disease model</i>		15	41.2	Bwtq6	body weight QTL 6
		15	49.6	Dbsty4	diabetesity 4

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Adenylosuccinate lyase (EC 4.3.2.2)	1494546	15	43.3		
Succinylpurinemic autism (MIM: 103050)					
<i>Linked to diet-induced disease model</i>		15	41.2	Bwtq6	body weight QTL 6
		15	49.6	Dbsty4	diabetesity 4

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
P450 progesterone 6 beta- and 16 alpha-hydroxylase	1659893	15	47.2		
Cyp2d10 (Many MIM)					
<i>Linked to diet-induced disease model</i>		15	49.6	Dbsty4	diabetesity 4

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Pou6f1	1795999	15	56.6		
Transcription (PMID: 8463278)					
<i>Linked to diet-induced disease model</i>		15	49.6	Dbsty4	diabetesity 4

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
BL1 inhibitor of proapoptotic protein BAX	1853004	15	56.8	(2 copies of the sequence)	
Inhibits apoptosis (MIM 600748)					
<i>Linked to diet-induced disease model</i>		15	49.6	<i>Dbsfy4</i>	<i>diabesity 4</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 16 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

MIM: Mendelian inheritance in Man information and number
GI_#: GenInfo number (Genbank identifier)
Chr: Chromosome number in mouse
CM: Centimorgan position in mouse
QTL_Name: Name of QTL
QTL Description: Describes QTL
Gene Function: QTLs that are +/- 10cM.
Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Protein Kinase DNA activating, PRKDC	1672875	16	9.2		
Regulates oncogene P53 and other transcription factors; involved in immunity (MIM 600899)					
<i>Linked to diet-induced disease model</i>		16	5	<i>Tanidd3</i>	<i>tally ho associated non-insulin dependent diabetes mellitus 3</i>
		16	14	<i>Bgeq15</i>	<i>body growth early QTL 15</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Zinc-finger transcription factor SLUG	2259460	16	9.4		
Transition of epithelial to mesenchymal (MIM 600748)					
<i>Linked to diet-induced disease model</i>		16	5	Tanidd3	tally ho associated non-insulin dependent diabetes mellitus 3
		16	14	Bgeq15	body growth early QTL 15

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Extracellular signal-regulated kinase 1 (EC 2.7.1.-)	2049576	16	9.82		
Maturation- or mitogen-activated protein (MAP) kinases. (MIM: 176948)					
<i>Linked to diet-induced disease model</i>		16	5	Tanidd3	tally ho associated non-insulin dependent diabetes mellitus 3
		16	14	Bgeq15	body growth early QTL 15

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Tricarboxylate transport protein.	1660257	16	10.7		
Movement of citrate across the mitochondrial inner membrane. (MIM: 190315)					
<i>Linked to diet-induced disease model</i>		16	5	Tanidd3	tally ho associated non-insulin dependent diabetes mellitus 3
		16	14	Bgeq15	body growth early QTL 15

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Homogentisate 1,2-dioxygenase (EC 1.13.11.5)	1699768	16	27.3		
Alkaptonuria: urine that turns dark on standing and alkalization, black ochronotic pigmentation of cartilage and collagenous tissues, and arthritis, especially characteristic in the spine. (MIM: 203500)					
<i>Linked to diet-induced disease model</i>		16	27.6	T2dm1	type 2 diabetes mellitus 1
		16	14	Bgeq15	body growth early QTL 15

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 17 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:** Mendelian inheritance in Man information and number
- GI_#:** GenolInfo number (Genbank identifier)
- Chr:** Chromosome number in mouse
- CM:** Centimorgan position in mouse
- QTL_Name:** Name of QTL
- QTL_Description:** Describes QTL QTLs that are +/- 10cM.
- Gene Function** Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Tubby super family protein; Tulp4	1937837	17	3.4		
Tubby causes insulin resistance, obesity. Membrane bound transcription factor involved in signal transduction (see: MIM 601197)					
<i>Linked to diet-induced disease model</i>		17	4	<i>Obq4</i>	<i>obesity QTL 4</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Pkd1: protein-protein and protein-carbohydrate interactions in the extracellular compartment	2075615	17	10.4		
Involved in renal function, mutations cause polycystic kidneys. Diabetics have increased renal complications (see: MIM 173900)					
<i>Linked to diet-induced disease model</i>		17	4	<i>Obq4</i>	<i>obesity QTL 4</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Vascular endothelial growth factor-3; VEGF-3	2057364	17	50.8		
Mitogen for vascular endothelial cells, Facilitate glucose passage across the blood-brain barrier in hypoglycemia (MIM 192240)					
<i>Linked to diet-induced disease model</i>		17	56.7	<i>Insq5</i>	<i>insulin QTL 5</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 18 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:** Mendelian inheritance in Man information and number
- GI_#:** GenInfo number (Genbank identifier)
- Chr:** Chromosome number in mouse
- CM:** Centimorgan position in mouse
- QTL_Name:** Name of QTL
- QTL_Description:** Describes QTL
- Gene Function:** QTLs that are +/- 10cM. Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Granulocyte colony-stimulating factor receptor	1373801	18	30		
Leukemias, granulopoiesis during the inflammatory process (MIM 138937)					
<i>Linked to diet-induced disease model</i>		18	28	<i>Bwq4</i>	<i>body weight, QTL 4</i>
		18	20	<i>Adip8</i>	<i>adiposity 8</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME 19 QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

- MIM:** Mendelian inheritance in Man information and number
- GI_#:** GenolInfo number (Genbank identifier)
- Chr:** Chromosome number in mouse
- CM:** Centimorgan position in mouse
- QTL_Name:** Name of QTL
- QTL_Description:** Describes QTL QTLs that are +/- 10cM.
- Gene Function** Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Tyrosine-protein kinase JAK2 (EC 2.7.1.112)	1487322	19	24		
Cytokine signaling, activates STAT5, often changed in certain cancers (MIM 147796)					
Linked to diet-induced disease model		19	26	Afw8	abdominal fat weight QTL 8

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Glycerol-3-phosphate acyltransferase	1807028	19	52		
Committed step in glycerolipid biosynthesis, regulation of cellular triacylglycerol and phospholipid levels, fasting/refeeding and administration of insulin caused a dramatic induction of GPAT (MIM 602395)					
Linked to diet-induced disease model		19	50	Tanidd1	tally ho associated non-insulin dependent diabetes mellitus 1
		19	51	Bglq13	body growth late QTL 13
		19	53	T2dm2	type 2 diabetes mellitus 2

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Transcription factor 7 - like	2308562	19	53		
T-cell specific, HMG-box and maps to Maps to bipolar disorder chromosomal location, other physiologies not excluded (MIM: 602272)					
<i>Linked to diet-induced disease model</i>		19	50	<i>Tanidd1</i>	<i>tally ho associated non-insulin dependent diabetes mellitus 1</i>
		19	51	<i>Bglq13</i>	<i>body growth late QTL 13</i>
		19	53	<i>T2dm2</i>	<i>type 2 diabetes mellitus 2</i>

GENES REGULATED BY DIET, GENOTYPE, OR GENOTYPE X DIET INTERACTIONS MAPPING TO CHROMOSOME X QTLs

QTL mapping is based upon statistical association and marker density. The closer the gene is to the QTL, the higher the probability of it being a candidate gene. The following tables provide:

MIM: Mendelian inheritance in Man information and number
GI_#: GenInfo number (Genbank identifier)
Chr: Chromosome number in mouse
CM: Centimorgan position in mouse
QTL_Name: Name of QTL
QTL Description: Describes QTL
Gene Function: QTLs that are +/- 10cM.
Based upon a variety of databases

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Iduronate 2-sulfatase (EC 3.1.6.13)	1428425	X	27		
Mucopolysaccharidosis II, mild form, Hunter's disease (MIM 309900)					
<i>Linked to diet-induced disease model I</i>		X	26.4	<i>Bw19</i>	<i>body weight QTL 19</i>
		X	17	<i>Afw11</i>	<i>abdominal fat weight QTL 11</i>

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Sodium and chloride dependent creatine transporter	2201454	X	29		
Creatine and creatine phosphate act as a buffer system for the regeneration of ATP in tissues with fluctuating energy demands (MIM 601294)					
<i>Linked to diet-induced disease model</i>		X	26.4	Bw19	body weight QTL 19

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Biglycan	1796473	X	29.3		
Chondrodysplasia punctata, may function to bind extracellular matrix and TGF beta, low bone density with age (MIM 310870)					
<i>Linked to diet-induced disease model</i>		X	26.4	Bw19	body weight QTL 19

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
DNA polymerase alpha catalytic subunit	1936838	X	34		
No disease association described (MIM 312040)					
<i>Linked to diet-induced disease model</i>		X	26.4	Bw19	body weight QTL 19

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Ephrin B1	1446754	X	37		
Eph family of receptor protein-tyrosine kinases, cell adhesion and aggregation (MIM 300035)					
<i>Linked to diet-induced disease model</i>		X	42	Bw12	body weight QTL 12

Gene Function	GI_#	Chr	CM	QTL_Name	QTL Description
Faciogenital dysplasia homolog, IG:Rho/Rac guanine nucleotide exchange factor;	2081188	X	64		
Autosomal dominant multiple physiologies (MIM 305400)					
<i>Linked to diet-induced disease model</i>		X	59.5	Dob7	<i>dietary obesity 7</i>

Fig 4. Diet-regulated Genes and Disease or Complex Phenotype Processes (alphabetical by function)

Key:

GI #: GenBank Number

Gene: Gene name

Function: Known or putative function

OMIM: On line Mendelian Inheritance in Man

PMID: PubMed ID Number

OMIM_Process: Summary of Process

OMIM_Detail: Description of function in disease from OMIM

GI #	Gene	Function	OMIM/PM	OMIM_Process	OMIM_Detail
1506585	Agpat1	1-acylglycerol-3-phosphate O-acyltransferase 1	MIM:603099	Metabolism	Also affects signal transduction processes
1905159	Rdh5	11-cis retinol dehydrogenase (EC 1.1.1.105)	MIM:601617	Signal_visual	Catalyze the conversion of 11-cis retinol to 11-cis retinal, final step in the biosynthesis of 11-cis retinaldehyde, the universal chromophore of visual pigments
1519882	Pbppd	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta (EC 3.1.4.11)	MIM: 601197	Obesity_Dibetes	Tubby binds to plasma membrane through 1-phosphatidylinositol-4,5-bisphosphate
1326479	Decr1	2,4-dienoyl-CoA reductase (NADPH2) (EC 1.3.1.34)	MIM:222745	Metabolism_lipids	metabolism of unsaturated fatty enoyl-CoA esters double bonds in both even- and odd-numbered positions; hyperlysinemia, hypocarnitinemia, a normal organic acid profile, and an unusual acylcarnitine
1738613	Trap2	Tumor necrosis factor receptor associated protein - Proteosome	MIM: 606223	Proteosome	Protein degradation
1649287	Ephx2	2-hydroxymuconic semialdehyde hydrolase (EC 3.7.1.9); Epoxide hydrolase (EC 3.3.2.3)	MIM:132811	Metabolism	
2050049	Prkfb1	6-phosphofructo-2-kinase (EC 2.7.1.105)	MIM:311790	Metabolism glycolysis	regulates Fructose 2,6-P(2) an allosteric activator of phosphofructokinase and glycolysis in liver and possibly in other tissues
1309170	Acacb	Acetyl-Coenzyme A carboxylase beta	MIM:601557	Metabolism	May decrease insulin sensitivity in muscle

1539949	Acat1	Acetyl-CoA acetyltransferase 1	MIM: 607809	Metabolism_Atherosclerosis	Involved in lipid metabolism
1650569	C1qbp	Acidic 82 kDa protein mRNA	MIM:601269	Immune Function	Complement C1q binding protein
1619179	Finb	Actin binding protein or transferring	MGI:1919025	Iron Transport	Anemia
2049046	Adk	Adenosine Kinase	MIM:102750	Metabolism_lipids	deficiency of adenosine metabolism contributes to the development of neonatal hepatic steatosis, a model postnatal lethal fatty liver.
2235102	Ak1	Adenylate kinase	MIM: 103000	Hemolytic Anemia	Involved in energy homeostasis
2181006	Adat1	Adenosine deaminase, tRNA	MIM: 604230	Cell function	Metabolism, produces ammonia, which may alter pH balance as in diabetes
1494546	Adsl	Adenylosuccinate lyase (EC 4.3.2.2)	MIM:103050	Autism	succinylpurinemic autism; some mutations: psychomotor retardation
1294347	Arfrp1	ADP-Ribosylation factor-related protein 1	MIM: 604699	Signal Transduction	GTP binding protein
1484064	AdipoR1	Adiponectin receptor 1	MIM: 607945	Diabetes	Adiponectin is a hormone secreted by adipocytes that regulates energy homeostasis and glucose and lipid metabolism
1908006	Akt2	Akt, Phosphoinositide-dependent serine-threonine protein kinase	MIM: 164731	Insulin Metabolism	mice deficient in Akt2 are impaired in the ability of insulin to lower blood glucose
1908636	Alb1	Albumin, serum Afamin,	MIM: 103600	Metabolism_lipids	Carrier protein for steroids, fatty acids, and thyroid hormones, stabilizes extracellular fluid volume; bisalbuminemia, occurs with overdose of beta-lactam antibiotics = acrocyanosis
1700965	Akr1A1	Alcohol dehydrogenase [NADP+] (EC 1.1.1.2)	MIM: 103830	Diabetes	Osmotic stress causes diabetic complications
1504171	Aldh3A2	Aldehyde dehydrogenase (EC 1.2.1.3)	MIM:270200	Metabolism_disease Diabetes	Sjogren-Larsson syndrome are those of congenital ichthyosiform erythroderma
2192713	Pdgfrl	Alpha platelet-derived growth factor receptor (EC 2.7.1.112)	MIM:604584	Signal_cancer	8p22-p21.3 that was commonly deleted in hepatocellular carcinoma (HCC), colorectal carcinoma and nonsmall cell lung carcinoma (NSCLC)
2042386	A2m	Alpha-2-macroglobulin	MIM: 103950	Alzheimers	alpha-2-macroglobulin, a serum pan-protease inhibitor, implicated in Alzheimer disease; mediates clearance and degradation of A-beta, the major component of amyloid beta deposits.
1744436	Tag	Alpha-galactosidase (EC 3.2.1.22)	MIM:301500	Metabolism_Fabry	Fabry disease, and OMIM: 104170,

						lysosomal storage
2308600	Als	Alsin		MIM: 606352	Amyotrophic lateral sclerosis	Mutations cause retrograde degeneration of the upper motor neurons of the pyramidal tracts
1446558	Anapc2	Anaphase-promoting complex sub 2		MIM: 603134	Cell Cycle	Cullin domain protein with ubiquitin domain involved in protein turnover which regulates processes like cell cycle control
2158093	Anapc5	Anaphase-promoting complex subunit 5		MIM: 606948	Cell Cycle	The anaphase-promoting complex (APC) consists of at least 8 protein subunits, including APC5, CDC27 (APC3), CDC16 (APC6), and CDC23 (APC8)
1309130	Agt	Angiotensinogen		MIM: 106150	Hypertension	may have a role in essential hypertension; T235 of AGT is an independent risk factor that carries an approximately 2-fold increased risk of coronary heart disease
1915779	Ank3	Ankyrin 3, epithelial		MIM:600465	Structure	Ankyrin-G is characteristically present at the axonal initial segment and nodes of Ranvier of neurons in the central and peripheral nervous systems.
1542232	Asf1b	Anti-silencing function		PMID: 12477932	Signal Transduction	Histone silencing domain
1807018	ApoB100	Apolipoprotein B100		MIM: 107730	Atherosclerosis_diseases	Familial hypobetalipoproteinemia (FHBL): autosomal dominant disorder lipid metabolism low plasma levels of apolipoprotein B & total- and low-density lipoprotein (LDL) cholesterol.
1446049	ATP1A4	ATPase, Na ⁺ /K ⁺ Transporting		MIM: 607321	Reproduction	Ouabain inhibition of Atp1a4 eliminated sperm motility
1752249	Aqp1	Aquaporin 1		MIM:107776	Transport_Signal	Aquaporin-CHIP is a 28-kD integral protein purified from the plasma membranes of red cells and renal tubules - binds to ephrinB receptor
1800393	Cbara1	Atopy related autoantigen CALC, Smhs2		MIM:605084	Allergy	Type 1 allergy
1655040	Atp5b	ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)		MIM:164360	Metabolism_energy	ATP synthase, multimeric complex at least 16 different polypeptides; 2 mitochondrially encoded
1650960	Psmc1	ATP-Dependent protease subunit		MIM:602706	Proteasome	20S catalytic proteasome and 2 PA700 regulatory modules, composed of multiple subunits, at least 6 related ATPases and ~15 non-ATPase polypeptides

2041641	Ddx10	ATP-Dependent RNA helicase DDX10	MIM:601235	Spliceosome_immune	ataxia-telangiectasia gene; immune defects, and a predisposition to malignancy; DEAD box proteins are putative RNA helicases that have a characteristic Asp-Glu-Ala-Asp
1556028	Atrn	Attractin precursor	OMIM:603130	Diabetesity	attractin was identified as the product of the murine 'mahogany' gene with connections to control of pigmentation and energy metabolism
1379831	Apg5l	Autophagy protein 5-like	MIM: 604261	Apoptosis	apoptosis specific protein contains a high number of acidic residues, a potential glycosylation site, and potential casein kinase II, protein kinase C, tyrosine kinase sites
1863019	Axin	Axin 1	MIM:603816	Signal_cancer	AXIN1 induced apoptosis in hepatocellular and colorectal cancer cells lacking APC, CTNNB1, or AXIN1. axin may suppress growth of hepatocellular and colorectal cancers
1909198	Tegt	Bax inhibitor-1	MIM:600748	Signal_apoptosis	BI1 suppressed apoptosis induced by BAX, etoposide, staurosporine, and growth factor deprivation, but not by FAS (CD95)
1284468	Catnb	Beta-catenin	MIM:116806	Signal_cancer	effector of intercellular adhesion, mutated in many cancers, involved in signal transduction pathways. an adherens junction protein
1796473	Bgn	Biglycan.	MIM:301870	Signal_apoptosis	may function in connective tissue metabolism by binding to collagen fibrils and TGF-beta promote neuronal survival
1542473	Tcra	Binding protein for T-cell receptor ;	MIM: 186880	Cancer_Leukemia	T-cell chronic lymphocytic leukemia MIM: 186960
1769161	Bing4	BING4 protein	MIM: 605660	Immune	A number of diseases are influenced by genes at the centromeric end of the major histocompatibility complex
1464229	Bpnt1	Bisphosphate 3'-nucleotidase 1	MIM:604053	Hypertension	resistance to salt;metal-dependent lithium-inhibited phosphomonoesterase; manic depression; lithium-induced nephrotoxicity (PMID: 10224133)
2158175	Bzw1	Basic leucine-zipper protein BZAP45	PMID: 11524015	Cell cycle	Histone 4 gene regulation
2140072	Bspry	A novel Ro-Ret protein	PMID: 10978534	Signal transduction	May be involved in cell transformation
2075615	Gli	C2H2 zinc finger transcription factor	MIM:165220	Signal_cancer	Basal cell carcinoma & Gli implicated in the

		JING				transduction of Sonic hedgehog - anendodermal signal that controls hindgut patterning and lung growth
2164107	Cabin1	Calcineurin inhibitor		MIM: 604251	Transcription	Involved in histone deacetylation processes
1310456	Camkk1	Calcium/calmodulin-dependent protein kinase I		MIM: 114080	Signal Transduction	Multifunctional and multipathway
1888270	S100a14	Calgizzarin; ERGO E-53		MIM: 603114	Signal_cancer	calgizzarin elevated in colorectal cancers compared with normal colorectal mucosa, one of several genes expressed in breast cancer-derived metastatic axillary lymph nodes but not in normal lymph nodes or breast fibroadenomas
1447096	Calm1	Calmodulin		MIM:114180	Signal_cell_cycle	growth and the cell cycle; signal transduction and the synthesis and release of neurotransmitters
1660476	Calm3	Calmodulin		MIM:114183	Signal_cell_cycle	include roles in growth and the cell cycle as well as in signal transduction and the synthesis and release of neurotransmitters
1862567	Calmbp1	Calmodulin-binding protein SHA1		PMID: 9819352	Signal_Cell_cycle	Sha1 (for spindle and hydroxyurea checkpoint abnormal),
1380860	Camta2	Calmodulin binding transcription activator 2		MIM: 139139	Signal Transduction	Immune function; apoptosis
1909356	Cldn14	Claudin 14		MIM: 605608	Deafness	Expressed in sensory epithelium of the organ of Corti
2187828	Cgef2-pending	cAMP-regulated guanine nucleotide exchange factor I		MIM: 606057	Signal	GEF(guanine nucleotide exchange factors) for RAP1A that is directly regulated by cAMP
2049140	Carm1	Coactivator of arginine methyltransferase		MIM: 603934	Cell regulation	Regulation of transcription
1310123	Ctss	Cathepsin S		MIM:116845	Immune	Cathepsins S and L play prominent roles in the degradation of the invariant chain (Ii, or CD74;
1555146	Ppap2a	Cavia porcellus phosphatidic acid phosphatase 2a		PMID: 10962286	Signal_lipids	MAY play an active role in the hydrolysis and uptake of lipids from the extracellular space
2248057	Cd59a	CD59A		MIM:107271	Anemia	restrict lysis of human erythrocytes and leukocytes by homologous complement, may be involved in Paroxysmal nocturnal hemoglobinuria - anemia
1650686	CentB1	Centaurin, beta		MIM: 607763	Cell function	Membrane recycling
1853138	Ccth	Chaperonin containing TCP-1 eta subunit		MIM: 605140	Cell metabolism	Assists the folding of newly translated polypeptide substrates through multiple

1529944	Ccr1	Chemokine receptor CCX CKR	MIM:606065	Signal	rounds of ATP-driven release and rebinding of partially folded intermediate forms
2308043	Trp53inp1	Transformation related protein 53 inducible nuclear protein 1	MIM: 193300	Signal_cancer	mediate activities through G protein-coupled receptors PMID: 10734104
2049793	Chi313	Chitinase, lectin gene family	PMID: 11297523	Immune Function	Regulated by P53
1359061	Ciks	CIKS (connection to IKK and SAPK/JNK) then to NFkB	MIM: 607043	Signal_transcription	Binds to GlcN oligosaccharides
1915216	Kras2	c-Ki-ras-1, hepatic	MIM: 190070	Signal_cancer	CIKS activates NFkB exclusively through an IKK-dependent mechanism.
1676738	Cln3	CLN3 protein	MIM:607042	Neuro/apoptosis	Oncogene, should be KRAS2, Krasa1 is a pseudogene Juvenile Batten: neurodegenerative disease,accelerated apoptotic death of photoreceptors and neurons. CLN3 and protein are overexpressed in a variety of human cancer cell lines
2284153	Myc	C-myc protein	MIM:113970	Cancer_apoptosis	Burkitt lymphoma: chromosomal translocations MYC gene and either the lambda or the kappa light chain immunoglobulin genes; induces S-phase and apoptosis
1497811	Copb1	Coatomer beta subunit	PMID: 11441537	Sorting	Hermansky-Pudlak syndrome characterized by the dysfunction of several subcellular organelles
2187172	Copb2	Coatomer beta subunit	MIM: 606990	Sorting	Golgi coatomer complex; constitutes the coat of nonclathrin-coated vesicles and is essential for Golgi budding and vesicular trafficking
1882128	CKN1	Cockayne syndrome group A	MIM: 216400	DNA Repair	Dwarfism, precociously senile appearance, pigmentary retinal degeneration, optic atrophy, deafness, marble epiphyses in some digits, photosensitivity, and mental retardation
1904767	Dpysl5	Collapsin response mediator protein 5 (Crmp5)	PMID: 10956643	Differentiation	Involved in neuronal growth control
1806950	C1s	C1sa: Complement C1s component precursor (EC 3.4.21.42)	MIM: 120580	Immune Function	Mutations associated with multiple pathologies
1483940	Cop1-pending	COP1 protein	MIM: 608067	Transcription	May regulate JUN, autoubiquination
1727163	Cox15	COX15 homolog	LL: 226139	Structure	Cytochrome c oxidase assembly protein

1357649	Rfx3	Cyclin G1 interacting protein	MIM: 601337	Transcription	transactivator of the human hepatitis B viral enhancer I
2200731	Gak	Cyclin G-associated kinase (EC 2.7.1.-)	MIM: 602052	Cell Cycle	Associates with cyclin G and CDK5
1649805	Ccnh	Cyclin H	MIM:601953	Signal_cell_cycle	CDK8 phosphorylation of cyclin H in vivo has a dominant-negative effect on cell growth. CAK= a 37-kD cyclin termed cyclin H and a 42-kD cyclin-dependent kinase CDK7
1504550	CcnM3	Cyclin M3	PMID: 12477932	Signal transduction	Involved in cell cycling?
1905747 2187717	Cars	CysteinyI-tRNA synthetase (EC 6.1.1.16)	MIM:123859	Protein synthesis	No known physiologies
2283227	Clic	Chloride transport, intracellular	PMID: 11997498	Singal_apoptosis	Interacts with P53
1910397	Cox5b	Cytochrome c oxidase, subunit Vb	MIM:123866	Metabolism_energy	terminal enzyme of the electron transport chain; 13 polypeptide subunits, 3 of which are encoded in mitochondrial DNA and 10 in nuclear DNA
2042539	Cyp11a	Cytochrome P450 11A1, mitochondrial precursor (EC 1.14.15.6)	MIM:118485	Metabolism	Steroid metabolism – many physiologies
1907861	Cyp2b9	Cytochrome P450 2B9 (EC 1.14.14.1)	PMID: 12130701	Steroid Metabolism	Testosterone 16a-hydroxylase, type a, mRNA increased in liver of diabetic obese mice
1902148	Cyp2c40	Cytochrome P450 2c40	PMID: 9721182	Metabolism_lipids	CYP2C40 produced an unidentified metabolite that coeluted with 16-, 17-, and 18-HETEs
1554316	Cyp4A3	Cytochrome P450 4A3 (EC 1.14.15.3); laurate omega-hydroxylase	PMID: 11513330	Metabolism_lipids	omega-hydroxylated fatty acids may have in cell signalling processes and as an alternative pathway for fatty acid metabolism
1555555	Cyp4B1	cytochrome P450 Cyp4b1	MIM: 124075	Detoxification	Oxidation of aromatic compounds
1659893	Cyp2d10	Cytochrome P450 monooxygenase; progesterone 6 beta- and 16 alpha-hydroxylation	PMID: 3219345	Steroid Metabolism	Any complex phenotype involving steroids
1445948	Dctd	dCMP deaminase	MIM: 607638	Metabolism	Precursors for DNA synthesis
2235239	Dbnl	Debrins	MIM:104610	Renal function	Amiloride binding protein – amiloride is a diuretic, sodium channel blocker
2187287	Rbp1	Deleted in split hand/split foot protein 1	MIM:180260	Metabolism_lipids	Carrier protein involved in the transport of retinol from the liver storage site to peripheral tissue.

1562575	Dld	Dihydrolipoamide dehydrogenase	MIM: 246900	Diabetes?	Lactic acidosis, ketoacidosis
1834201	1600017E01 Rik	Dihydrolipoamide succinyltransferase.	MIM:126063	Metabolism_disease	Machado-Joseph disease as another candidate for mutation in the DLST gene.
1862437	Dhodh	Dihydroorotate dehydrogenase	MIM: 126064	Metabolism_nucleotides	Involved in pyrimine biosynthesis
1554403	Dpep1	Dipeptidase (EC 3.4.-.-)	MIM:179780	Antibiotics	RDP is responsible for hydrolysis of the beta-lactam ring of antibiotics such as penem and carbapenem
1841125	NP_659138.1	dJ545L17.3 (proteasome (prosome, macropain) inhibitor subunit 1 (P131)	MIM: 602855	Proteosome	Proteosome component
1497664	Dnmt1	DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37)	MIM:126375	Signal_transcription	Abnormalities of DNA methylation occur consistently in human neoplasia; binds proliferating cell nuclear antigen, an auxiliary factor for DNA replication and repair
1676114	Dffa	DNA fragmentation factor, 45 kD, alpha polypeptide	MIM:601882	Apoptosis	protein that induces DNA fragmentation in coincubated nuclei after it is activated by caspase-3
2308561	Ruvbl2	DNA helicase	MIM: 604788	Cell Function	Replication, repair, and transcription
1936838	Pola1	DNA polymerase alpha catalytic subunit	MIM: 310465	Cancer_visual	Visual impairment, deafness, laterally overlapping upper eyelids, large corneas, abnormal auricles, cryptorchidism, hypospadias and spasticity; lymphoblastic leukemia
1684156	Rpc62	DNA-directed RNA polymerase III, subunit 4 (EC 2.7.7.6)	MIM:604892	Transcription	GTF3C4 = TFIIIC90, 2 potential zinc finger motifs at the C terminus, GTF3C4 has intrinsic histone acetyltransferase activity.
1542146	Xrcc1	DNA repair protein XRCC1	MIM: 194360	Cancer	DNA repair
1904320	Dpm2	Dolichyl-phosphate-mannose--protein mannosyltransferase (EC 2.4.1.109)	MIM: 603564	Metabolism_lipids	DPM2 is not essential for Dol-P-Man synthase activity; however, the presence of DPM2 significantly increases the specific enzymatic activity
1505147	Dntnp	Dosal neuron-tube nuclear protein	PMID: 11984880	Cell Function	Biochemical function unknown
1902535	Dfy	Duffy antigen/receptor for chemokine glycoprotein	MIM: 110700	Immune Function	Binds IL8 and may be malaria receptor
1318275	Gcn511	Dynamin-like 120 kDa protein (GCN5)	MIM:601444	Signal_amino_acids	GCN4 protein activates transcription of a large number of amino acid biosynthetic genes under limiting amino acid conditions
1371927	Dnclc1	Dynein light chain 1, Outer arm	MIM: 601562	Signal	DLC1 protein physically interacts with and inhibits the activity of neuronal NOS

1282761	Dnclc2	Dynein 2 light intermediate chain	PMID: 8812413	Structure	Dyneins are microtubule-associated motor protein complexes composed of several heavy, light, and intermediate chains.
2283419	Mta1l1	Echinoderm microtubule-associated protein-like 4	MIM:603947	Transcription	Associated with NuRD, a multisubunit complex containing nucleosome remodeling and histone deacetylase
1702212	Lre1	Endonuclease/reverse transcriptase	MIM: 151626	DNA repair?	Mobile genetic element, DNA repair?
1357618	Serpinf1	EPC-1 - serpin, = serine protease inhibitor; Pigment epithelium-derived factor precursor	MIM: 172860	Signal_angiogenesis	PEDF inhibited endothelial cell migration (dose-dependent) the most potent natural inhibitors of angiogenesis
1446754	Efnb1	Ephrin B1	MIM:300035	Signal Transduction	Protein receptor tyrosine kinase
1557815	Trim25	Estrogen-responsive finger protein	MIM:600453	Signal_cell_cycle	RING-finger-dependent ubiquitin ligase (E3) that targets proteolysis of 14-3-3-sigma a negative cell cycle regulator that causes G2 arrest.
1328562	Elf2b	Eukaryotic translation initiation factor 2B, subunit 2	MIM: 606454	Translation	Eukaryotic initiation factor-2B (EIF2B) is a GTP exchange protein essential for protein synthesis; leukoencephalopathy with vanishing white matter
2049576	Mapk1	Extracellular signal-regulated kinase 1 (EC 2.7.1.-)	MIM:176948	Signal_cancer	ERKs are also known as maturation- or mitogen-activated protein (MAP) kinases
1465081	F11r	jCam1	MIM: 605721	Structure	Ligand for the integrin LFA1; a platelet receptor - inferred
2081188	Fgd1	Faciogenital dysplasia homolog, IG:Rho/Rac guanine nucleotide exchange factor	MIM:305400	Signal_development	ocular hypertelorism, anteverted nostrils, broad upper lip, and peculiar penoscrotal relations ('saddle-bag scrotum' or 'shawl scrotum').
2042313	Fbxo6	F-box protein FBX6b	MIM: 605647	Signal_apoptosis	Component of modular E3 ubiquitin protein ligases
2292384	Fdx1	Ferredoxin, 2Fe-2s; ERGO: E-25	MIM:103260	Metabolism_energy	small, acidic, iron-sulfur protein that functions as an electron transport intermediate for mitochondrial cytochromes P450 involved in steroid, vitamin D, and bile acid metabolism.
2256866	Fn1	Fibronectin precursor	MIM:135600	Cancer_structure	Domains for heparin, collagen, cells, hyaluronic acid, heparin, C1 binding. Ehlers-Danlos syndrome (type X), required for metastasis
2042203	Foxn1	Forkhead box n1	MIM: 600838	Immune_Alopecia	Winged helix nude: alopecia and immunodeficiency
1630486	SFRP4	Frizzled-related protein 4	MIM: 606570	Signal_apoptosis	paracrine WNT/frizzled signaling is inhibited

					by SFRPs in overloaded myocardium; inhibition is associated with depletion of cytosolic beta catenin & the induction of apoptosis
1746733	Ccne1	G1/S-specific cyclin E1	MIM:123837	Signal_Cancer	breast cancers, as well as some other solid tumors, show severe quantitative and qualitative alterations in cyclin E protein production.
1475428	Ccnf	G2/mitotic-specific cyclin F	MIM:600227	Proteosome	ubiquitin proteolysis through Skp1 and Skp2
1487297	Gabpb1	GA-binding protein transcription factor, beta subunit 1	MIM:600610	Trancription	transcriptional regulation of a number of subunits of mitochondrial enzymes, including cytochrome c oxidase
1882008	Galt	Galactose-1-phosphate uridyl transferase ;	MIM: 230400	Metabolism_disease	large liver, icterus, failure to thrive, and urinary excretion of albumen and sugar, mental developmental problems
2102585	Gsn	Gelsolin	MIM: 137350	Structure metabolism	familial amyloidosis, Finnish type-disrupted calcium binding in D2 makes the domain a target for aberrant proteolysis the first step in the cascade
1861211	Ugt1a1	Glucuronosyltransferase (EC 2.4.1.17) precursor	MIM: 218800	Metabolism_disease	nonhemolytic jaundice with kernicterus; hyperbilirubinemia
1811443	Gls	Glutaminase (EC 3.5.1.2), hepatic, NO ERGO	MIM:138280	Cancer	GAC is also the predominant isoform expressed in a breast cancer cell line with high glutamine consumption.
1807028	Gpam	glycerol-3-phosphate acyltransferase mRNA, .	MIM: 602395	Metabolism_lipids	highly expressed in lipogenic tissues, such as liver and adipose tissue. In animal studies, fasting/refeeding and administration of insulin caused a dramatic induction of GPAT
1355364	Pygb	Glycogen phosphorylase (EC 2.4.1.1), brain	MIM:138550	Metabolism_disease	1,4-D-glucan:orthophosphate D-glucosyltransferase - liver; 232700 glycogen storage disease
2262484	Golph1	Golgi phosphoprotein 3	PMID: 11042173	Protein Transport	Many physiological processes and diseases
1897200	Gosr1	Golgi SNAP receptor complex member 1	MIM: 604026	Protein Transport	Golgi functions
1373801	Csf1r	Granulocyte colony-stimulating factor receptor	MIM:164770	Cancer_Leukemia	hemopoietic growth factor receptor gene may be important in the pathogenesis of myeloid leukemia also
1488749	Ghr	Growth hormone secretagogue receptor type 1	MIM:600946	Signal_hormone	Laron syndrome; growth hormone insensitivity syndrome (GHIS)

1853004	Tegt	Growth hormone-inducible membrane protein	MIM:600748	Apoptosis	BI1 suppressed apoptosis induced by BAX, etoposide, staurosporine, and growth factor deprivation, but not by FAS (CD95)
1913128	Ghim	Growth hormone-inducible membrane protein	PMID: 11416014	Energy metabolism	GH-agonist induces brown adipose tissue
2164939	Gna11	Guanine nucleotide binding protein, alpha 11	MIM:139313	Signal_development	Gnaq and Gna11 have overlapping functions in embryonic cardiomyocyte proliferation and craniofacial development
1542354	Gna13	Guanine nucleotide binding protein	PMID: 8999798	Signal transduction	Angiogenesis
1317824	Gngt2	Guanine nucleotide binding protein, gamma transducing activity polypeptide 2	MIM:603655	Signal_visual	G protein gamma subunit, G-gamma-c (previously named G-gamma-8), which may play a key role in coupling the cone visual pigment to phosphodiesterase.
1751874	Gbp2	Guanylate binding protein	MIM:600412	Signal	GBPs bind guanine nucleotides (GMP, GDP, and GTP) and are distinguished from the GTP-binding proteins by the presence of 2 binding motifs rather than
1464733	Ubr1	Hect-domain ubiquitin protein ligase E3 (EC 6.3.2.-)	MIM:605981	Cell Functon	RCC1-like G exchanging factor-like protein; Regulator of chromosome condensation
1446915 1776367	Hemgn	Hemogen	PMID: 11404085	Transcription?	Novel nuclear protein involved in hematopoiesis
1514269	Hba	Hemoglobin alpha chain	MIM:141800	Physiology	Thalassemias
1505258	Hs6st1	Heparan sulfate 6-O-sulfotransferase 1	MIM: 604846	Structural enzyme	Sulfation of anosmin is involved in Kallmann syndrome, a congenital, isolated, idiopathic hypogonadotropic hypogonadism and anosmia (lack of smell).
1895338	Hal	Histidine ammonia-lyase (EC 4.3.1.3); histidase	MIM: 235800	Metabolism_neuro	Histidinemia is a benign metabolic disorder that does not require treatment
1676239	Hdc	Histidine decarboxylase (EC 4.1.1.22)	MIM:142704	Signal	biogenic amine histamine is an important modulator of numerous physiologic processes, including neurotransmission, gastric acid secretion, and smooth muscle tone.
1501085	Bat8	HLA associated transcript; NG36 protein	PMID: 12586828	Transcription	May be involved in methylating histone G9a
1901249	Ssh3bp1	HNap1 binding protein	MIM: 603050	Signal transduction	ABI1 plays a role in the leukemogenesis by translocating to MLL (mixed lineage leukemia). May increase c-Abl protein kinase activity

2196139	Hnrph3	hnRNP 2H9A	MIM:602324	Spliceosome	Ribonucleoprotein (RNP) complexes consisting of hnRNAs and associated proteins are responsible for RNA splicing and processing.
1531123	Hipk2	Homeodomain-interacting protein kinase 2 (EC 2.7.1.-)	MIM: 606868	Signal_Cancer	colocalizes and interacts with p53 and CREB-binding protein
1699768	Hgd	Homogentisate 1,2-dioxygenase (EC 1.13.11.5)	MIM:203500	Transport	manifestations: urine that turns dark on standing and alkalization, black ochronotic pigmentation of cartilage and collagenous tissues, and arthritis, especially in spine.
2305949	Flot1	HSPC154 protein = flotillin?	MIM: 606998	Structure	Integral membrane protein, may be associated with caveolins, which are found in all cells, but especially adipocytes
1283303	Hip1	Huntingtin interacting protein 1	MIM:601767	Apoptosis	HIP1: membrane-associated protein colocalizes with huntingtin with sequence homology and biochemical characteristics with Sla2p, functions in the cytoskeleton; apoptosis
1497254	Hmgcs2	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5)	MIM:600234	Metabolism_energy	ketogenesis, a metabolic pathway that provides lipid-derived energy for brain, heart, kidney, and other organs during times of carbohydrate deprivation, such as fasting
2288264		Hypothetical 50.0 kDa protein		Structure	Single-stranded nucleic acid binding R3H, chromosome position known
1428425	Ids	Iduronate 2-sulfatase (EC 3.1.6.13)	MIM: 309900	Metabolism_lipids	Mucopolysaccharidosis II: iduronate sulfatase deficiency, hepatosplenomegaly from mucopolysaccharide deposits, cardiovascular disorders
1487422	Ier5	Immediate early response 5	MIM: 607177	Metabolism	Responds to addition of serum (none in quiescent state)
1915278	IMAP38	Immunity associated immune function	MIM: 608084	Structure	Endoplasmic reticulum protein
1487112	Pyp	Inorganic pyrophosphatase (EC 3.6.1.1)	MIM:179030	Metabolism	Involved in driving pyrophosphate releasing reactions to completion
2192375	Itpk1	Inositol 1,3,4-trisphosphate 5/6 kinase	MIM:601838	Metabolism	Signal transduction processes
1297504	Itgb1bp1	Integrin cytoplasmic domain-associated protein 1	MIM: 607153	Structure	Suggested that ICAP1 plays an important role in integrin-dependent cell adhesion.
1755563	lag203	Interferon activated gene 203	IPR004020	Inflammation and Signal transduction	Pyrin domain was identified as putative protein;protein interaction domain at the N-terminal region of several proteins thought to function in apoptotic and inflammatory

							signaling pathways
1889604	Il6ra	Interleukin 6 receptor, alpha	MIM:147880	Signal_immune			regulation of the immune response, hematopoiesis, and acute-phase reactions
1500921	JM11	JM11 protein	PMID: 11138001	Immune			immune homeostasis
1795172	DXImx38e	JM5 protein 125kd membrane protein	PMID: 12477932	Unknown			WD40 domain, adaptor/regulatory modules in signal transduction, pre-mRNA processing and cytoskeleton assembly
1372685	Jmj	Jumonji; repressor of cyclin D	PMID: 12852854	Neurogenesis			Involved in neural tube formation
1357656	Kns2	Decahistidyl-kinesin light chain	MIM:600025	Cell Function			Molecular motors that move tubulin and chromosomes
1555484	Kif21b	Kinesin family member 21B	PMID: 10225949	Cell Function			Molecular motors, also involved in neuron function
2306066	Kpnb1	Karyopherin (Importin)	PMID: 9369227	Intracellular transport			May play a role in differentiation and organogenesis
1509303	Lamb2	Laminin, beta 2	MIM: 150325	Nephrotic Syndrome?			cell differentiation, adhesion, migration, and neurite outgrowth
1644096	Cyp43	Laurate omega-hydroxylase (EC 1.14.15.3) cytochrome P450 4A5	PMID: 2766933	Kidney function			May play an important role in the regulation of blood pressure and renal function during pregnancy
1658728	Mrc2	Lectin lambda protein	PMID: 8702911	Immune_Structure			Cell adhesion and immune function
1643870	Vip36 Lman2l	Lectin, mannose binding	SWISSPROT (Q12907)	Cell structure			Endoplasmic reticulum protein
1285968	Lars	Leucyl tRNA synthetase	MIM: 151350	Protein synthesis			Charges leucine onto tRNA
1509296	Lgn	LGN	PMID: 11832491	Signal Transduction			Cytoplasmic regulators of G-protein signaling
1284318	Lbp	Lipopolysaccharide-binding protein	MIM: 151990	Immune			Lipopolysaccharide-binding protein is an acute-phase reactant produced during gram-negative bacterial infections.
1861663	Es1	Liver carboxylesterase 22 precursor (EC 3.1.1.1)	MIM: 605278	Metabolism			CES2 specifically catalyzes the hydrolysis of the benzoyl group of cocaine and the acetyl groups of 4-methylumbelliferyl acetate, heroin, and 6-monoacetylmorphine
1555767	Ly6g6c	Lymphocyte antigen 6 complex	MIM: 606038	Signal transduction			Protein attached to cell membrane
1650046		LYST-interacting protein LIP5	PMID: 8349643	Metabolism_lipids			involved in lipoic acid metabolism; yeast KO LIP5 gene slow growth on ethanol-rich media and barely detectable growth on glycerol-rich media.

1861860	1700020D05 Rik	Mage-g2	MIM: 300341	Cancer	expressed in melanomas and other cancers
2057364	Ppm1b	Magnesium dependent protein phosphatase	MIM:603770	Signal_cancer	absolute requirement for magnesium or manganese and its insensitivity to the tumor promoter okadaic acid.
1932173	Mup2	Major urinary protein 2 precursor	PMID: 3600652	Transport	MUPs are synthesized in at least six secretory tissues under a variety of developmental and endocrine controls
1853320	Map1lc3	MAP1 light chain 3-like protein 1	MIM: 157130	Structure	microtubule-associated proteins (MAPs) isolated from brain coassemble with tubulin into microtubules in vitro
2187377	PPP3CA	Map kinase phosphatase-M A1 isoform	MIM: 114105	Signal transduction	Many physiological processes, including memory functions
1282018	Camk2b	MCAMK1-BETA2 protein	MIM:607707	Signal_neuro	Calcium/calmodulin regulated protein kinases.
2041342	Timp3	Metalloproteinase inhibitor 3 precursor, extracellular matrix	MIM:188826	Structure_dystrophy	Sorsby fundus dystrophy: central (macular) lesion showing edema, hemorrhage, and exudates.
1294487	Gst2	Microsomal glutathione S-transferase 2	MIM: 601733	Signal_lipids	GST2 gene is associated with cell microsomes and can catalyze the production of LTC4 (leukotrienes) from LTA4 and reduced glutathione.
1527865	Mcrs1	Microspherule protein 1	PMID: 11709724	Transcription	Nucleolar protein that directly interacts with the ICP22 regulatory protein from herpes simplex virus 1 or with p120, a proliferation-related protein expressed at high levels in most human malignant tumor cells
2288329	Slc25a20	Mitochondrial carnitine/acylcarnitine carrier protein	MIM:212138	Metabolism_lipids	Mitochondrial oxidation of fatty acids: chief source of energy during prolonged fasting and for skeletal muscle during exercise and for cardiac muscle. DIET; apnea
2235265	Mtch2- pending	Mitochondrial carrier homolog 2	IPR001993	Metabolism	Transport of solutes across mitochondria
1558135	5730405E07 Rik	Mitochondrial intermediate peptidase (EC 3.4.24.59)	MIM: 602241	Signal_neuro	Friedreich ataxia: neurodegenerative disease typically caused by deficiency of frataxin; which interacts with the peptidase. Iron accumulation
1875338	Mrps2	Mitochondrial ribosomal protein S2	MIM 607118	Cancer	labeled as 2, reports 3 - transcript overexpressed in a hepatocellular carcinoma (HCC) infected with hepatitis B virus - Important?

1529619	Rps27	Mitochondrial ribosomal protein S27	MIM: 603702	Protein synthesis	Identified in ERGO database
1474933	Mrps30	Mitochondrial ribosomal protein S30	PMID: 10874039	Protein Synthesis	Identified in EGO database
1711797	M-Ras	M-Ras GTPase	PMID: 9395237	Structure	Reorganization of the cytoskeleton
1375545 2040121	Myadm	Myeloid associated differentiation	PMID: 10733104	Immune function	Myeloid differentiation
1795994	Dscr1	Myocyte-enriched calcineurin interactin protein 1 splice variant 4	MIM: 190685	Down's Syndrome	Down's syndrome
1464684	Myh9	Myosin heavy chain, fast skeletal muscle, embryonic	MIM:160775	AD_macrothrombocytopenia	autosomal dominant macrothrombocytopenia with leukocyte inclusions
1840637	Myipc	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MIM:160781	Atherosclerosis	regulation of myosin ATPase activity in smooth muscle; rare variant of cardiac hypertrophy as well as abnormal skeletal muscle
1660028	Myo5a	Myosin Va	MIM:160777	Signal_cell_cycle	myosin V function in the centrosome of human lymphocytes may be essential either for cellular proliferation or for the polarized movement of the centrosome that occurs during T-killer or T-helper cell response
1937664	Slc9a1	NA(+)/H(+) exchanger 1	MIM:107310	Hypertension	pH regulation of vertebrate cells
1934380	Ndufs5	NADH-ubiquinone oxidoreductase 13 kDa B subunit (EC 1.6.5.3) / NADH dehydrogenase (EC 1.6.99.3)	MIM:603848	Energy Metabolism	Multisubunit NADH:ubiquinone oxidoreductase (complex I) is the first enzyme complex in the electron transport chain of mitochondria.
1407501	NdufsX	NADH-ubiquinone oxidoreductase subunit B17.2 (EC 1.6.5.3) / NADH dehydrogenase (EC 1.6.99.3)	MIM:603322 ?	Energy metabolism	Multisubunit NADH:ubiquinone oxidoreductase (complex I) is the first enzyme complex in the electron transport chain of mitochondria.
1555757	Mell1	Neprilysin-like peptidase gamma	PMID: 10749671	Protease	Metalloprotease, sequence similar to mel oncogene
2271912	Mme	Neprilysin-like peptidase gamma	MIM:120520	Alzheimers	downregulation of neprilysin activity, which could be caused by aging, can contribute to Alzheimer disease by promoting amyloid-beta accumulation
1325306	Ncald	Neurocalcin delta	MIM: 606722	Signal transduction	Neuronal signal transduction process
1435837	Nefl	Neurofilament, light polypeptide	MIM: 162280	Structure	Cytoplasmic intermediate filaments (IF)
1513763	Lrrn3	Neuronal leucine-rich repeat protein-3	PMID: 9011764	Structure	Development and maintenance of neuron function
1285745	Nab2	NGFI-A binding protein 2 (EGR1-	MIM: 602381	Transcription	Repress EGR1 and EGR2, zinc finger

		binding protein 2)			transcription factors encoded by immediate-early genes, implicated in a wide variety of proliferative and differentiative processes.
2202141	Noelin	Noelin 3 precursor			
1290045	N-ras	N-ras protein	PMID: 2835730	Oncogene	Involved in signal transduction
2250161	Nscn1	Non-selective cation channel 1			
2292188	Numa	Nuclear mitotic apparatus protein 1	MIM: 164009	Sorting	NUMA fragment also specifically interacts with the nuclear transport factor, importin-beta, fused to RARA in Acute myelocytic leukemia (APL)
2186532	Nrbp	Nuclear receptor binding protein	PMID: 11956649	Signal Transduction	Interacts with Ras GTPase, serine/threonine kinase domain
2288782	Nol5a	Nucleolar protein Nop56	PMID: 12571235	Transcription	Processing RNA
1355494	Ncl	Nucleolin; RHUM120913 4e-56	MIM:164035	Signal	abundantly expressed acidic phosphoprotein of exponentially growing cells and is located mainly in dense fibrillar regions of the nucleolus
1474962	Nme2	Nucleoside diphosphate kinase (EC 2.7.4.6)	MIM: 156491	Metastasis Inhibition	May act in the regulation of signal transduction by complexing with G proteins, causing activation/inactivation of developmental pathways
2049524	Nulp1	Nuclear localized binding protein	PMID: 12107429	Transcription	Helix-loop-helix protein
1446725	Osr1	Odd-skipped related 1 protein	PMID: 12386165	Oxidative Stress	Interacts with cation chloride transport
1380090	Slc22a12	Organic cation transporter protein 2	MIM:602631	Beckwith-Wiedman	Enlarge organs, also hypoglycemia
2199776 2076093	Oazi	Ornithine decarboxylase antizyme	PMID: 10623564	Proteosome	ODC, in association with AZ, is degraded by the 26S proteasome in an ATP-dependent, but ubiquitin-independent, manner.
2041096	Osgp	O-sialoglycoprotein endopeptidase (EC 3.4.24.57)	PMID: 12039036	Extracellular	Adhesion, immune function?
2041160	Ott-Mal	OTT-MAL	MIM: 606077	Cancer_Leukemia	The recurrent t(1;22)(p13;q13) translocation is exclusively associated with infantile acute megakaryoblastic leukemia
1447198	Pard6A	Partitioning defective protein	MIM: 607484	Signal transduction	Regulates cell polarity
1539108	pPIE	Peptidyl-prolyl cis-trans isomerase E (EC 5.2.1.8)	MIM: 604486	Metabolism	Cyclophilins, also referred to as rotamases, catalyze the cis to trans isomerization of certain proline imidic peptide bonds in

						oligopeptides,	
1427567	Tpo	Peroxidasin: Thyroid peroxidase precursor (EC 1.11.1.8)	MIM: 274500	Metabolism		discharge of a significant percentage of labeled iodide from the thyroid upon administration of thiocyanate or perchlorate,	
1463760	Ptdsr	Phosphatidylserine receptor PtdSerR	MIM:604914	Phagocytosis		Clearance of apoptotic cells	
1356924	Pde6d	3',5'-cyclic phosphodiesterase delta-subunit (EC 3.1.4.17), Retinal rod rhodopsin-sensitive cGMP	MIM:602676	Signal		The delta subunit (PDE6D) seems to play a role in stabilizing the catalytic dimer from membranes	
1765588	Plscr3	Phospholipid scramblase 3	MIM:604170	Apoptosis		Increase in intracellular calcium due to cell activation, cell injury, or apoptosis causes a rapid bidirectional movement of the plasma membrane PLs between leaflets: agglutination	
2142939	Ppp1cp	Phosphoprotein phosphatase (EC 3.1.3.16) 1-beta catalytic chain	PMID: 2544298	Signal transduction		Calceineurin family	
1505093	Dusp7	Phosphatase, dual specificity 7	PMID: 11310585	Cancer		Induced by Pten,	
1540342	Al481750	PIPPin protein	PMID: 12767259	RNA processing		RNA binding motifs	
1436592	Vipr2	Pituitary adenylate cyclase-activating polypeptide (PACAP)	PMID: 8146174	Insulin		may participate in the regulation of insulin secretion	
1316383	Pkwa	Pkwa (EC 2.7.1.-) Serine/threonine-protein kinase	PMID: 11101684	Protein:protein interactions		Similarity to Thermomonospora curvata CCM3352 serine/threonine protein kinase with WD40 domain	
1529387	Ptn	Pleiotrophin	PMID: 12107166	Signal Transduction		Accessory signaling molecular involved in bone formation	
1530447	Pmx	Pmx homeobox gene similar to U03873	MIM: 167420	Development		Skeletal development	
1862676	Parn	Poly(A)-specific ribonuclease	MIM:604212	Spliceosome		PARN is a 3-prime exonuclease that prefers poly(A) as the substrate	
2075615	Pckd1	Polycystic kidney disease gene	MIM: 173900	Kidney		Protein-protein and protein-carbohydrate interactions in extracellular compartments	
1744344	Pmscl2	Polymyositis/scleroderma autoantigen	MIM:605960	Cell function		Ribonuclease D (EC 3.1.26.3)	
1902592	Pfdn2	Prefoldin subunit 4	MIM: 604898	Structure_sorting		heterohexameric chaperone protein, which they called prefoldin. One of its subunits, prefoldin-4, is identical to C1.	
1795999	Pou6f1	POU transcription factor	PMID: 8463278	Transcription		Homology	
1317814	Prnpip1	Prion protein interacting protein 1; KAPD -	IPR006055	Unknown		Exonuclease	

1644107		B. subtilis, kinase					
	Cymp	Prothymosin (EC 3.4.23.4)	MIM:118943	Milk digestion	Aspartyl protease		
1938196	Pcolce2	Procollagen C-endopeptidase enhancer 2; ERGO E-37	MIM: 607064	Metabolism_lipids	N-terminal signal sequence, 2 CUB domains, and an NTR domain. It also contains a putative myristoylation site, several potential phosphorylation sites, a putative glycosylation site, and an RGD site		
1476573	Prlr	Prolactin receptor	MIM:176761	Signal_reproduction	mammalian reproduction		
1328575	P4hb	Protein disulfide-isomerase (EC 5.3.4.1)	MIM:176790	Diabesity	Also known as glutathione-insulin transhydrogenase, it catalyzes thiol:protein-disulfide interchange.		
1672875	Prkdc	Protein Kinase DNA activating subunit Myotrophin	MIM:600899	Immune_Cancer	VDJ recombination, interacts with P53		
1542413	Prkcbp	Protein kinase (EC 2.7.1.37) N beta	MIM: 605926	Signal_neuro	protein interacting with C kinase-1 regulates glutamate receptor		
1796404	TarA	Protein Tara	J:64118	Proteosome	paternally expressed ubiquitin-specific processing protease		
1426777	Eif3	Protein Translation Initiation Factor 3 (IF-3)	MIM: 602039	Translation	EIF3 has been implicated in several roles, including binding to the 40S ribosomal subunit - 8 subunits		
1681368	Eif5	Protein Translation Initiation Factor 5B (IF-5B)	MIM:601710	Translation	Eukaryotic translation initiation factor 5 (EIF5) interacts with the 40S initiation complex to promote hydrolysis of bound GTP with concomitant joining of the 60S ribosomal subunit to the 40S initiation complex.		
2232491	Fes	Proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112)	MIM:190030	Immune_Cancer	FES has a role in regulating the innate immune response		
1474562	Nori-2	Prpk - P53 related protein kinase	PMID: 11546806	Signal transduction	P53 related protein kinase		
2199927	Pycr1	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	MIM: 179035	Metabolism	Catalyzes the NAD(P)H-dependent conversion of pyrroline-5-carboxylate to proline.		
1554726	Gdi1	RAB GDP dissociation inhibitor alpha	MIM:300104	Mental Retardation?	Signal transduction, interacts with CDC42, geranylgeranyl of CDC42 binds with Gdi1 and releases it from the membrane		
2284221	Rab11b	RAB11b, member RAS oncogene family	MIM:604198	Signal	Small GTPase mediated signal transduction		
1542583	Rin1	Ras and Rab interactor 1	MIM:605965	Signal Transduction	Endocytosis, cytoskeleton		
2288598	Rgi2	Ral guanine nucleotide dissociation stimulator-like 2	MIM: 605667	Signal	Ral guanine nucleotide dissociation stimulator (RALGDS) and its family members		

						are involved in Ras and Ral signaling pathways as downstream effector proteins.
2071849	Reps1	RALBP1 associated Eps domain containing 1		PMID: 93954471175 0063	Signal	Ras-RalGDS signal transduction pathway.
1826093	Rara	Retinoic acid receptor alpha		MIM:180240	Transcription	Retinoic acid is a vitamin A metabolite
2187647	Iqgap1	Ras GTPase-activating-like protein IQGAP1		MIM:603379	Signal	Ras-related GTPase-activating (RasGAP) family of proteins. 6 copies of a unique motif and 4 IQ motifs (tandemisoleucine and glutamine residues), modulate binding with calmodulin
1767997	Sara	RasGAP-activating-like protein 2		MIM:605401	Signal	homolog of SAR1 yeast
1711970	Plxnc1	Receptor for viral-encoded semaphorin protein		MIM:604259	Immune	from the Plexin C OMIM: plexin may be an immune modulator during virus infection.
1318639	Recc1	Replication factor C large subunit		MIM:102579	Cell_cycle_replication	DNA-dependent ATPase that binds in a structure-specific manner to the 3-prime end of a primer hybridized to a template DNA, expressed in 28 of 30 samples of acute myelogenous leukemia; 9 of 11 samples of adult acute lymphoblastic leukemia, all cases tested of (CML) in blast crisis;
1841024	Rgs2	RGS2-like protein		MIM:600861	Cancer_Leukemia	Ribonuclease
1474741	Rib1	Ribonuclease III (EC 3.1.26.3)		MIM:180440	Cell Function	Removes the 5-prime leader sequences from precursor tRNA molecules, same as POP4, processing of precursor gene from S. cerevisiae
1426774	Rp929	Ribonuclease P protein subunit p29		MIM:606114	Splicesome	Mammalian ribosome is a macromolecular assembly of 4 RNA species and 80 proteins
1808466	Rpl27a	Ribosomal protein L27a		MIM:603637	Structure	Ribosomal protein
1436776	Rps18	Ribosomal protein S18		MIM:180473	Protein synthesis	Mice deficient for S6 kinase-1, effector of the phosphatidylinositol-3-OH kinase signaling pathway, are hypoinsulinemic and glucose intolerant; pancreatic mass lower (type 2)□
2308493	Rps6ka1	Ribosomal protein S6 modification protein		MIM:601684	Diabetesity	Mitochondrial protein synthesis
1541068	Mrpl2	Ribosomal protein, mitochondrial, L2		PMID: 10593885	Protein synthesis	Similar to B-Raf protooncogene
1309316	Rmil	RMIL serine/threonine-protein kinase (EC 2.7.1.37)		PMID: 1620546	Cancer	Inferred function, no physiology
1865332	Rbm14	RNA binding motif protein 14 (inferred)		PMID: 12477932	RNA processing	insulin treatment of both cell types was found
1659436	Paf53-	RNA polymerase I-associated factor		PMID:	Diabetesity	

	pending	PAF53 (EC 2.7.7.6)	9688843		to increase the nuclear content of upstream binding factor (UBF) and RNA polymerase I-associated factor 53
2186858	Tceb1l	RNA Polymerase II TF SIII	MIM:600695	Transcription	may be involved in transcription regulation for the development or maintenance of specialized functions of the inner ea
2075437	Neurod1	Rod1	MIM:601724	Diabetes	2 heterozygous mutations in NEUROD1 which were associated with the development of type II diabetes
1316119	S100a15	S100 calcium-binding protein A15	PMID: 12923069	Psoriasis	S100 protein is produced by a wide variety of normal and neoplastic cells of mesodermal, neuroectodermal, and epithelial origin
1542150	Sardh	Sarcosine dehydrogenase (EC 1.5.99.1)	MIM:268900	Metabolism_neuro	ARDH is defective in patients with sarcosinemia; mild mental retardation and few other abnormalities
1699511	Sec13r	SEC13, Protein transport protein	MIM: 600152	Cell function	Intracellular protein transport and sorting
1287847	Sema4a	Semaphorin 4A precursor	MIM:607292	Structure	Semaphorins (SEMA)s are a family of transmembrane and secreted proteins that appear to function during growth cone guidance.
1862318	Sema4g	Semaphorin subclass 4 member G	PMID: 10495281	Structure	Axon guidance
1446873	Sep3	Septin 3; GTPases	PMID: 10446280	Signal_development	embryogenesis and in adult tissues
1659713	Serpina3n	Serine protease inhibitor 2	PMID: 12127095	Signal_transcription	SPI-3 mRNA-positive pineal cells-translocation of the signal transducers and activators of transcription 3 (STAT3) into nuclei after lipopolysaccharide injection.
2250230	Spink4	Serine protease inhibitor Kazal-type 4 sp P00998	MIM:167790	Diabetes	Proteinaceous inhibitors of serine proteases. Spink1 involved in hereditary or idiopathic chronic pancreatitis
1650732	Serpina6	Serine proteinase inhibitor NK13	MIM:173321	Signal_apoptosis	developmentally regulated; implicated in the regulation of tumor progression, inflammation, and cell death.
1649379	BC011468	Serine/Threonine protein kinases	IPR000719	Signal transduction	Serine/threonine kinase domain
2164199	Rad53	Serine/threonine-protein kinase Chk2 (EC 2.7.1.-)	MIM:151623	Cancer	Li-Fraumeni - highly penetrant familial cancer. ATM--CHK2--CDC25A--CDK2 pathway as a genomic integrity checkpoint that prevents radioresistant DNA synthesis
2049985	Saa	Serum amyloid A-2 protein precursor	MIM: 104751	Immune	acute phase reactant serum amyloid A is a

						polymorphic apolipoprotein
1875865	Shc1	Shc transforming protein	MIM: 600560	Signal_apoptosis		A regulator of Forkhead transcription, involved in life span and apoptosis
2057851	Sharpin	Sharpin; shank interacting protein	PMID: 11178875	Neuronal function		Interacts with the ankyrin repeats of Shank at postsynaptic density of excitatory neurons
2042146	Scoc	Short Coiled coil protein SCOCO	PMID: 11303027	Unknown		Proteins with this motif are involved in protein sorting and Golgi interactions
1908569	Skiip	SKI interacting protein	MIM:603055	Transcription		With coactivator GRIP1, the coregulator Ski-interacting protein (SKIP)/NCoA-62 synergistically enhance ligand-dependent VDR transcriptional activity
1325565	Snrpd2	Small nuclear ribonucleoprotein Sm D2	MIM: 601061	Signal_autoimmune		SNRNPs : primary autoantigens for the anti-Sm antibodies produced by patients with lupus erythematosus
2307889	Sip1	SMN interacting protein 1-gamma	OMIM:602595	Splicesome_atrophy		MN-SIP1 complex is associated with spliceosomal snRNAs U1; survivor of motor neuron, mutated in 98% of all spinal muscular atrophy
1644037	Snrk	SNF-1 related kinase	MIM: 605705	Metabolism_control		SNF1 and the acetyltransferase GCN5 function in an obligate sequence to enhance INO1 transcription by modifying histone H3 serine-10 and lysine-14.
2201454	Creat	Sodium and chloride dependent creatine transporter	MIM: 300036	Metabolism_energy		Creatine-phosphocreatine shuttle has important functions in the temporal and spatial maintenance of the energy supply to skeletal and cardiac muscle
1391034	Slc2a6	Solute carrier family 2, facilitated glucose transporter, member 8	MIM:606813	Diabesity		Glucose transporter
1699506	Slc22a7	Solute carrier family 22 (Organic anion transporter), member 7	MIM:604995	Transport		located in the sinusoidal membranes of hepatocytes, bidirectional transport of organic anions
1649568	Snx12	Sorting nexin 12	PMID: 11102511	Sorting		retromer complex, involved in retrograde transport of proteins from endosomes to the trans-Golgi network
1285920	Snx5	Sorting nexin 5	MIM: 605937	AR_sorting		SNX5 expression affects FANCA -Fanconi pancytopenia: AR affects all bone marrow elements. associated with cardiac, renal, and limb malformations and dermal pigmentary changes.
1530059	Spnb1	β -Spectrin	MIM:182070	Anemia		Red cell membrane structural protein

2073633	Spin	Spindlin	PMID: 9053325	Signal_Cell_cycle	suggest that spindlin plays a role in cell-cycle regulation during the transition from gamete to embryo.
1675453	Sf3b1	Splicing factor 3B subunit 1	MIM:605590	Spliceosome	Spliceosome component: U2 snRNP -12S unit and 2 splicing factors, SF3A, composed of 3 proteins & SF3B, which is composed of 4 proteins.
2308907	SPOP	Speckled type POZ protein	MIM: 602650	Transcription	Involved in transcription or splicing
1861831	Spp30	SPP30	PMID: 10561073	Unknown	Cell surface protein
1794458	Sart1	Squamous cell carcinoma antigen recognized by T-cells 1	MIM:605941	Growth	suggesting preferential expression in proliferating cells.
1937187	Nssr	SRRP35 - splicing	MIM:605221	Spliceosome_immune	TASR exhibit opposing effects on adenovirus E1A pre-splicing and abrogate the influence of TLS on this splicing; strongly expressed in peripheral blood leukocytes
1905127	Biklk	SSX2 interacting protein hRabin3A, isoform beta2	MIM: 603392	Signal_apoptosis	BIK promoted cell death in a manner the BCL2-related death-promoting proteins BAX
1676097	Stk2	Ste20-related kinase SMAK	MIM: 601959	Signal transduction	Serine/threonine protein kinase 2
1662193	Mln64	Steroidogenic acute regulatory protein	MIM:600617	Metabolism steroids	nonsense mutations in the STAR gene can cause lipoid congenital adrenal hyperplasia; mediates the rapid increase in pregnenolone synthesis stimulated by tropic hormones.
1861959	Cyp27a1	Sterol 26-hydroxylase (EC 1.14.-.-), VitD Cyp27A	MIM: 213700	Metabolism atherosclerosis	Cerebrotendinous xanthomatosis rare, inherited lipid-storage disease neurologic dysfunction, premature atherosclerosis, and cataracts. Vitamin D
1875374	Stra13	Stra13	PMID: 11890681	Cell function	Inhibits cell cycle progression
1554874	Sep1	Strand exchange protein - exoribonuclease	MIM: 607994	Cell functions	RNA degradation, telomere function, recombination
1287118	Mknk1	Stress-activated map kinase interacting protein 1: Mknk1	MIM: 606724	Signal_stress	MNK1 interacts with the eIF4F complex, Mnk1 enzymatically activated in response to mitogenic and stress stimuli.
1671585	SUPV3L1	Suppressor of var-1	MIM: 605122	Control of respiration	Mitochondrial RNA helicase protein
1677535	Spk	Symplekin	MIM:602388	Cell Structure	cytoplasmic face of the tight junction-containing zone (zonula occludens) of polar epithelial cells and Sertoli cells of the testis
1752493	Cd1d1	T-cell surface glycoprotein CD1d1 precursor	MIM:188410	Diabesity	CD1D, a ligand for CD8(+) T cells, on human intestinal epithelial cells (IECs); CD1d-null

1464182	Tcte1			T-complex-associated-testes-expressed-1	MIM:186975	Transcription	NOD transgenic mice: accelerated onset and increased incidence of diabetes compared +/- and +/- littermates
2042203	Tde1l			TMS-2 membrane protein	PMID: 10637174	Unknown	normal tail length, embryogenesis, and spermatogenesis
1494921	Tebp			Telomerase binding protein p23	PMID: 12135483	Aging	Neuron specific
1427550	Tnmd			Tenomodulin	PMID: 11162640	Dementia, Cancer	Involved in synthesizing telomeres, short telomeres result in cell death
1715326	D7Rp2e			Testosterone-regulated RP2 protein	PMID: 1766361	Unknown	Electron transport activity
1650417	Slc22a1l			Tetracycline transporter-like protein	MIM:602631	Cancer	loss of heterozygosity in the lung cancer; tumor suppressor gene in the fetal kidney
2158359	Slc12a3			Thiazide-sensitive NaCl cotransporter	MIM: 600968	Hypertension	Na+, Cl- transporter
1937851	Nssr			TLS (translocated in liposarcoma)-associated protein TASR-2	MIM:605221	Spliceosome_immune	TASR exhibit opposing effects on adenovirus E1A pre-splicing and abrogate the influence of TLS on this splicing; strongly expressed in peripheral blood leukocytes
2042025	Nssr			TLS-associated protein TASR-2	MIM:605221	Spliceosome_immune	TASR exhibit opposing effects on adenovirus E1A pre-splicing and abrogate the influence of TLS on this splicing; strongly expressed in peripheral blood leukocytes
1309228	Tasp			Toll associated serine protease	Unpublished	Signal transduction	Toll receptors are integral membrane proteins involved in cell signalling
1793885	Tor2a			Torsin family 2, member A	MIM:128100	Dystonia_Structure	Dystonia' involuntary, sustained muscle contractions; 'torsion' refers to the twisting nature of body movements observed in dystonia.
1861831	Trappc5			Trafficking protein particle complex 5 (putative)	PMID: 11217851	Vesicle trafficking	All physiological processes including atherosclerosis
2292059	Taldo1			Transaldolase (EC 2.2.1.2)	MIM:602063	Metabolism_energy	key enzyme of the pentose phosphate pathway, which is responsible for generation of reducing equivalents to protect cellular integrity from reactive oxygen intermediates.
1861530	Tcea1			transcription elongation factor TFIIIS.oB	MIM: 604784	Transcription	Releases RNA polymerase from transcriptional arrest
1538938	Tcfap2c			Transcription factor AP-2, gamma	MIM:601602	Signal_cancer	regulate the expression of genes required for development of tissues of ectodermal origin such as neural crest and skin and breast

						cancer
2308562	Tcf7l2	Transcription factor 7-like 2, T-cell specific, HMG-box	MIM: 602272	Transcription		Maps to bipolar disorder chromosomal location, other physiologies not excluded
1752241	Zfp162	Transcription factor ZFM1	PMID: 9660765	Transcription_Cancer		ZFM1 repress transcription transcription factor, stage-specific activator protein (SSAP), EWS, a human protein in Ewing's sarcoma tumors
1282149	Gtf2a1	Transcription initiation factor IIA alpha and beta chains	MIM:600520	Transcription		Transcription was dramatically reduced in cells following immunodepletion of TFIIA/alpha and could be restored by addition of TFIIA/alpha.
1677308	TbpMIM:600075	Transcription initiation factor TFIID subunit	MIM:600075	AD_truncal ataxia		truncal ataxia, spasticity, and muscle weakness caused by expansion of polyglutamate region. Autosomal dominant
2164720	Trmprs2	Transmembrane protease, serine 2 (EC 3.4.21.-)	MIM:602060	Atherosclerosis_diabesity		four domain protein: domain (3) is an LDL receptor class A (LDLRA) domain (this type of domain forms a binding site for calcium); movement of citrate across the mitochondrial inner membrane
1660257	Slc25a1	Tricarboxylate transport protein	MIM:190315	Metabolism_lipids		
1908150	Trim	Tripartite motif containing protein, may be an E3 ubiquitin ligase	MIM: 602290	Muscular dystrophy		May also be involved in AIDS (HIV infection)
1749050	Trim21	Tripartite motif containing protein Sjogren syndrome antigen A1: SSA1	MIM: 109092	Autoimmunity		Ribonucleoprotein complex involved in Sjogren syndrome and Systemic Lupus Erythematosus
1446182	Amd1	S-adenosyl methyltransferase	MIM:180980	Cancer		Related to tRNA (Uracil-5-) - methyltransferase (EC 2.1.1.35) - similarity
1530862	Pus1	tRNA pseudouridine synthase A (EC 4.2.1.70)	PMID: 10094309	Protein synthesis		Involved in tRNA processing
1937837	Tulp4	Tubby super-family protein (Tusp)	PMID: 11595174	Obesity_Diabetes		Mutations in tubby cause obesity
1903941	Mid1	Tubulin--tyrosine ligase (EC 6.3.2.25)	MIM:300000	Proteosome_development		midline abnormalities cleft lip, laryngeal cleft, heart defects, hypospadias, and agenesis of the corpus callosum; E3 ubiquitin ligase activity PPC; PP2CA accumulates
1487322	Jak2	Tyrosine-protein kinase JAK2 (EC 2.7.1.112)	MIM:147796	Signal_hormone		constitutively associated with the prolactin receptor (PRLR),STAT5 is activated in a broad spectrum of human hematologic malignancies.
1553927	Snrp70	U1 Small nuclear ribonucleoprotein 70 KD	MIM: 180740	Splicesome_autoimmune		human U1-70K snRNP protein is the major antigen recognized by anti-(U1)RNP sera from patients with autoimmune diseases

1699544	Btrc	U3 snoRNP-associated 55-kDa protein	MIM:603482	Signal	data suggest that BTRCP and SKP1 components of an ER-associated protein degradation pathway that mediates CD4 proteolysis, includes IFKb, beta catenin, reg by axin
1284184	Snrfp	Small nuclear ribonucleoprotein polypeptide F	MIM: 603541	RNA Splicing	U6 snRNA-associated Sm-like protein LSM6
2164616	Lsm7	U6 snRNA-associated Sm-like protein LSM7	MIM:607287	RNA Splicing	By homology to yeast, decapping of mRNA and exonuclease Xrn1
1793047	Usp18	Ubiquitin carboxyl-terminal hydrolase (EC 3.1.2.15)	MIM:607057	Signal_immune	Expression regulated during cytokine-induced monocytic cell differentiation. Overexpression blocked cytokine-induced terminal monocytic differentiation; reg by A-5A and RNaseL
2257369	Usp18	Ubiquitin carboxyl-terminal hydrolase (EC 3.1.2.15)	MIM:607057	Signal_immune	Expression regulated during cytokine-induced monocytic cell differentiation. Overexpression blocked cytokine-induced terminal monocytic differentiation; reg by A-5A and RNaseL
1895437	Usp18	Ubiquitin carboxyl-terminal hydrolase 4 (EC 3.1.2.15)	MIM:607057	Signal_immune	Expression regulated during cytokine-induced monocytic cell differentiation. Overexpression blocked cytokine-induced terminal monocytic differentiation; reg by A-5A and RNaseL
2157776	Uchl5	Ubiquitin carboxyl-terminal hydrolase isozyme L5 (EC 3.4.19.12)	MIM:191342	Parkinson's	Proteosomal protein degradation
1543807	Unc93b	unc93 (C.elegans) homolog B	PMID: 9798653	Muscle function?	Muscle contraction in C. elegans – induced by IL4 in B cells
1554068	Vps45	Vacuolar protein sorting 45	PMID: 8996080	Sorting	vesicle trafficking between the Golgi apparatus, prelysosomal compartment(s), and the lysosome.
2187159	Vegfa	Vascular endothelial growth factor-3; VEGF-3	MIM:192240	Signal_angiogenesis	only mitogen that specifically acts on endothelial cells, major regulator of tumor angiogenesis in vivo, candidate hormone for facilitating glucose passage across the blood-brain barrier under critical conditions
1476080	Vat1	Vesicle amine transport	MIM: 604631	Brain function	Neurotransmitter function
1447666	Vav2	VAV2 protein	MIM:600428	Signal transduction	Surface receptor tyrosine kinases
2102226	Vilp	Villin-like protein	MIM: 153615	Structure	higher molecular weight than gelsolin and a very restricted tissue distribution, being found only in intestinal microvilli and renal tubular

2262509	Vdac1	Voltage dependent ion channel	MIM: 193245	Metabolism_Structure	epithelial cells
1896487	Wee1	Wee1 Tyrosine kinase	MIM: 193525	Signal transduction	Binds hexokinase, may be involved in apoptosis
1436657	Wbscr5	Williams-Beuren Syndrome gene	MIM: 605719	Immune function	A cell cycle regulatory gene
1355012	Wrch1	WNT1-responsive CDC46 analog	MIM: 606366	Structure	B cell, but syndrome has multiple phenotypes
2202207	Whsc2h	Wolf-Hirschhorn syndrome candidate 2 protein	MIM:606026	Signal_development	Regulation of cell morphology, cytoskeletal organization, and cell proliferation severe growth retardation and mental defect, microcephaly, 'Greek helmet' facies, and closure defects (cleft lip or palate, coloboma of the eye, and cardiac septal defects).
2283540	Pdcd2	Zinc finger protein 189	MIM:600866	Cancer_apoptosis	homolog of Rp8, a rat gene associated with programmed cell death in thymocytes, lymphomas
1464723	Slc25a17	Solute carrier family 25	MIM: 606795	Transport	Colocalizes with peroxisomal thiolase
2076192	Zfp358	Zinc finger protein ZFEND	PMID: 12036583	Transcription	Transcription
2073725	Zfp393	Zinc finger protein	PMID: 12351194	Reproduction	May be involved in spermatid differentiation and oocyte development
1649248	Agtpbp1	Zinc-carboxypeptidase precursor	MIM:606830	Neuro	nna1 as the gene mutated in the Purkinje cell degeneration (pcd) phenotype of mouse
2259460	Snai2	Zinc-finger transcription factor SLUG	MIM:602150	Signal_development	conversion of pluripotent epithelial derivatives into various neural crest derivatives require complex cellular and environmental interactions modulated by lineage-specific transcription factors.